

0989575-070504

Gag_AF110965_BW_mod

ATGGGCGCCCGCGCCAGCATCCTGCGCGGGCGGCAAGCTGGACGCCTGGGAGCGCATCCGCC
TGCGCCCCGGCGGCAAGAAGTGCTACATGATGAAGCACCTGGTGTGGGCCAGCCGCGAGCT
GGAGAAGTTCCGCCCTGAACCCCGGCCCTGCTGGAGACCAGCGAGGGCTGCAAGCAGATCATC
CGCCAGCTGCACCCCGCCCTGCAGACCGGCAGGAGGAGCTGAAGAGCCTGTTCAACACCCG
TGGCCACCCTGTACTGCGTGACGAGAAGATCGAGGTCCGCGACACCAAGGAGGCCCTGGA
CAAGATCGAGGAGGAGCAGAACAAGTGCCAGCAGAAGATCCAGCAGGCCGAGGCCGCCGAC
AAGGGCAAGGTGAGCCAGAATAACCCATCGTGCAAGCCTGCAGGGCCAGATGGTGCACC
AGGCCATCAGCCCCCGCACCCTGAACGCCTGGGTGAAGGTGATCGAGGAGAAGGCCTTCAG
CCCCGAGGTGATCCCCATGTTACCGCCCTGAGCGAGGGCGCCACCCCCCAGGACCTGAAC
ACGATGTTGAACACCGTGGGCGGCCACAGGCCGCCATGCAGATGCTGAAGGACACCATCA
ACGAGGAGGCCGCCGAGTGGGACCGCGTGACCCCGTGACGCCGGCCCCATCGCCCCCGG
CCAGATGCGCGAGCCCCGCGGCAGCGACATCGCCGGCACCACCAGCACCCCTGCAGGAGCAG
ATCGCCTGGATGACCAGCAACCCCCCATCCCCGTGGGCGACATCTACAAGCGGTGGATCA
TCCTGGGCCTGAACAAGATCGTGCGGATGTACAGCCCCGTGAGCATCCTGGACATCAAGCA
GGGCCCCAAGGAGCCCTTCCGCGACTACGTGGACCGCTTCTTCAAGACCCCTGCGCGCCGAG
CAGAGCACCCAGGAGGTGAAGAACTGGATGACCGACACCCCTGCTGGTGCAGAACGCCAACC
CCGACTGCAAGACCATCCTGCGCGCTCTCGGCCCGCGGCCAGCCTGGAGGAGATGATGAC
CGCCTGCCAGGGCGTGGGCGGCCCCAGCCACAAGGCCCGCGTGCTGGCCGAGGCGATGAGC
CAGGCCAACACCAGCGTGATGATGCAGAAGAGCAACTTCAAGGGCCCCCGGCGCATCGTCA
AGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCCGCAACTGCCGCGCCCCCGCAAGAA
GGGCTGCTGGAAGTGCGGCAAGGAGGGCCACCAGATGAAGGACTGCACCGAGCGCCAGGCC
AACTTCCTGGGCAAGATCTGGCCCAGCCACAAGGGCCGCCCCGGCAACTTCCTGCAGAGCC
GCCCGAGCCCAACCGCCCCCCCCCGCGAGAGCTTCCGCTTCGAGGAGACCACCCCGGCCA
GAAGCAGGAGAGCAAGGACCGCGAGACCCTGACCAGCCTGAAGAGCCTGTTGGGCAACGAC
CCCCTGAGCCAGTAA

Figure 1

09899575.070504

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ATGGGCGCCCGCGCCAGCATCCTGCGCGGCGAGAAGCTGGACAAGTGGGAGAAGATCCGCC
TGGCCCCCGGCGGCAAGAAGCACTACATGCTGAAGCACCTGGTGTGGGCCAGCCGCGAGCT
GGAGGGCTTCGCCCTGAACCCCGGCCTGCTGGAGACCGCCGAGGGCTGCAAGCAGATCATG
AAGCAGCTGCAGCCCCGCCCTGCAGACCGGCACCGAGGAGCTGCGCAGCCTGTACAACACCG
TGGCCACCCTGTACTGCGTGCACGCCGCGCATCGAGGTCCGCGACACCAAGGAGGCCCTGGA
CAAGATCGAGGAGGAGCAGAACAAGTCCCAGCAGAAGACCCAGCAGGCCAAGGAGGCGGAC
GGCAAGGTGAGCCAGAACTACCCCATCGTGCAGAACCTGCAGGGCCAGATGGTGCACCAGG
CCATCAGCCCCCGCACCCCTGAACGCCTGGGTGAAGGTGATCGAGGAGAAGGCCTTCAGCCC
CGAGGTGATCCCCATGTTTACCGCCCTGAGCGAGGGCGCCACCCCCCAGGACCTGAACACG
ATGTTGAACACCGTGGGCGGCCACCAGGCCGCCATGCAGATGCTGAAGGACACCATCAACG
AGGAGGCCCGCCGAGTGGGACCGCCTGCACCCCGTGCAGGCCCGGCCCGTGGCCCCCGGCCA
GATGCGCGACCCCCGCGGCAGCGACATCGCCGGCGGCCACCAGCACCCCTGCAGGAGCAGATC
GCCTGGATGACCAGCAACCCCCCGTGCCCGTGGGCGACATCTACAAGCGGTGGATCATCC
TGGGCCCTGAACAAGATCGTGGGATGTACAGCCCCGTGAGCATCCTGGACATCCGCCAGGG
CCCCAAGGAGCCCTTCGCGGACTACGTGGACCGCTTCTTCAAGACCCCTGCGCGCCGAGCAG
GCCACCCAGGACGTGAAGAACTGGATGACCGAGACCCCTGCTGGTGCAGAACGCCAACCCCG
ACTGCAAGACCATCCTGCGCGCTCTCGGCCCGCGGCCACCCCTGGAGGAGATGATGACCGC
CTGCCAGGGCGTGGGCGGCCCCGGCCACAAGGCCCGCGTGCTGGCCGAGGCGATGAGCCAG
GCCAACAGCGTGAACATCATGATGCAGAAGAGCAACTTCAAGGGCCCCCGGCGCAACGTCA
AGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCAAGAACTGCCGCGCCCCCGCAAGAA
GGGCTGCTGGAAGTGGGCAAGGAGGGCCACCAGATGAAGGACTGCACCGAGCGCCAGGCC
AACTTCCTGGGCAAGATCTGGCCCAGCCACAAGGGCCCGCCCCGGCAACTTCCTGCAGAACC
GCAGCGAGCCCGCCGCCCCCAACGTGCCACCGCCCCCCCCCGCCGAGAGCTTCCGCTTCGA
GGAGACCACCCCCGCCCCCAAGCAGGAGCCCAAGGACCGCGAGCCCTACCGCGAGCCCCTG
ACCGCCCTGCGCAGCCTGTTCGGCAGCGCCCCCTGAGCCAGTAA

Figure 2

Fig. 3

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--> signal peptide (1-81)
ATGCGCGTGATGGGCATCCTGAAGAACTACCAGCAGTGGTGGATGTGGGGCATCTGGGCTTCTGGATGCTGATCA
TCAGCAGCGTGGTGGGCAACCTGTGGGTGACCGTGTACTACGGCGTGCCCGTGTGGAAGGAGGCCAAGACCACCCT
GTTCTGCACCAGCGACGCCAAGGCCTACGAGACCGAGGTGCACAACGTGTGGGCCACCCACGCCTGCGTGCCACCC
GACCCCAACCCCCAGGAGATCGTGCTGGAGAACGTGACCGAGAACTTCAACATGTGGAAGAACGACATGGTGGACC
AGATGCACGAGGACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGCTGACCCCCCTGTGCGTGAC
CCTGAAGTGCCGCAACGTGAACGCCACCAACAACATCAACAGCATGATCGACAACAGCAACAAGGGCGAGATGAAG
AACTGCAGCTTCAACGTGACCACCGAGCTGCGCGACCGCAAGCAGGAGGTGCACGCCCTGTTCTACCGCCTGGACG
TGGTGCCCTGACAGGGCAACAACAGCAACGAGTACCGCCTGATCAACTGCAACACCAGCGCCATCACCCAGGCCTG
CCCCAAGGTGAGCTTCGACCCCATCCCCATCCACTACTGACCCCCGCGGCTACGCCATCCTGAAGTGCAACAAC
CAGACCTTCAACGGCACCGGCCCTGCAACAACGTGAGCAGCGTGAGTGCGCCACGGCATCAAGCCCGTGGTGA
GCACCCAGCTGCTGCTGAACGGCAGCCTGGCCAAGGGCGAGATCATCATCCGCAGCGAGAACCTGGCCAACAACGC
CAAGATCATCATCGTGAGCTGAACAAGCCCGTGAAGATCGTGTGCGTGCGCCCCAACAACAACACCCGCAAGAGC
GTGCGCATCGGCCCCGGCCAGACCTTCTACGCCACCGCGGAGATCATCGGCGACATCCGCCAGGCCTACTGCATCA
TCAACAAGACCGAGTGAACAGCACCCTGCAGGGCGTGAGCAAGAAGCTGGAGGAGCACTTCAGCAAGAAGGCCAT
CAAGTTCGAGCCCAGCAGCGGCGGCGACCTGGAGATCACCAACACAGCTTCAACTGCCGCGGCGAGTTCTTCTAC
TGCGACACCAGCCAGCTGTTCAACAGCACCTACAGCCCCAGCTTCAACGGCACCGAGAACAAGCTGAACGGCACCA
TCACCATCACCTGCCGCATCAAGCAGATCATCAACATGTGGCAGAAGGTGGGCCGCGCCATGTACGCCCCCCCCAT
CGCCGGCAACCTGACCTGCGAGAGCAACATCACCGGCCTGCTGCTGACCCGCGACGGCGGCAAGACCGGCCCAAC
GACACCGAGATCTTCCGCCCCGGCGGCGGCGACATGCGCGACAACCTGGCGCAACGAGCTGTACAAGTACAAGGTGG
TGGAGATCAAGCCCTGGGCGTGCCCCCACCAGGCCAAGCGCCGCGTGGTGGAGCGCGAGAAGCGCGCCGTGGG
CATCGGCGCCGTGTTCTGGGCTTCCTGGGCGCCGCGGCGAGCACCATGGGCGCCGCCAGCATCACCTGACCGTG
CAGGCCCCCTGCTGCTGAGCGGCATCGTGACGAGCAGACAACCTGCTGCGCGCCATCGAGGCCAGCAGCACC
TGCTGCAGCTGACCGTGTGGGGCATCAAGCAGCTGCAGACCCGCATCTGGCCGTGGAGCGCTACCTGAAGGACCA
GCAGCTGCTGGGCATCTGGGGCTGCAGCGGCAAGCTGATCTGCACCACCGCCGTGCCCTGGAACAGCAGCTGGAGC
AACCGCAGCCACGACGAGATCTGGGACAACATGACCTGGATGCAGTGGGACCGCGAGATCAACAACCTACACCGACA
CCATCTACCGCCTGCTGGAGGAGAGCCAGAACCAGCAGGAGAAGAACGAGAAGGACCTGCTGGCCCTGGACAGCTG
GCAGAACCTGTGGAATGGTTTCAGCATCACCAACTGGCTGTGGTACATCAAGATCTTCATCATGATCGTGGGCGGC
CTGATCGGCCTGCGCATCATCTTCGCCGTGCTGAGCATCGTGAACCGCGTGCGCCAGGGCTACAGCCCCCTGCCCT
TCCAGACCCTGACCCCAACCCCCGCGAGCCCGACCGCCTGGGCGGCATCGAGGAGGAGGGCGGCGAGCAGGACCG
CGGCCGAGCATCCGCTGCTGAGCGGCTTCCTGGCCCTGGCCTGGGACGACCTGCGCAGCCTGTGCTGTTTACG
TACCACCGCCTGCGCGACTTCATCTGATCGCCGCCCGCGTGTGGAGCTGCTGGGCCAGCGCGGCTGGGAGGCC
TGAAGTACCTGGGCAGCCTGGTGCACTACTGGGGCTGGAGCTGAAGAAGAGCGCCATCAGCCTGCTGGACACCAT
CGCCATCGCCGTGGCCGAGGGCACCGCATCATCGAGTTTCATCCAGCGCATCTGCCGCGCCATCCGCAACATC
CCCCCGCATCCGCCAGGGCTTCGAGGCCGCCCTGCAGTAA

Fig. 4

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--> signal peptide (1-72) \/-->
ATGCGCGTGCGCGGCATCCTGCGCAGCTGGCAGCAGTGGTGGATCTGGGGCATCCTGGGCTTCTGGATCTGCAGCG
gp120/140/160 (72)
GCCTGGGCAACCTGTGGGTGACCGTGTACGACGGCGTGCCCGTGTGGCGCGAGGCCAGCACCACCCTGTTCTGCGC
CAGCGACGCCAAGGCTACGAGAAGGAGGTGCACAACGTGTGGGCCACCCACGCCCTGCGTGCCCAACCGACCCCAAC
CCCCAGGAGATCGAGCTGGACAACGTGACCGAGAACTTCAACATGTGGAAGAACGACATGGTGGACCAGATGCAAG
AGGACATCATCAGCCTGTGGGACCAGAGCCTGAAGCCCCGCGTGAAGCTGACCCCCCTGTGCGTGACCCTGAAGTG
CACCAACTACAGCACCAACTACAGCAACACCATGAACGCCACCAGCTACAACAACAACACCACCGAGGAGATCAAG
AACTGCACCTTCAACATGACCACCGAGCTGCGCGACAAGAAGCAGCAGGTGTACGCCCTGTTCTACAAGCTGGACA
TCGTGCCCTGAACAGCAACAGCAGCGAGTACCGCCTGATCAACTGCAACACCAGCGCCATCACCAGGCCTGCC
CAAGGTGAGCTTCGACCCCATCCCCATCCACTACTGCGCCCCCGCGGCTACGCCATCCTGAAGTGCAAGAACAAC
ACCAGCAACGGCACCGGCCCTGCCAGAACGTGAGCACCCTGCACTGCAACCCACGGCATCAAGCCCGTGGTGAGCA
CCCCCTGCTGCTGAACGGCAGCCTGGCCGAGGGCGGCGAGATCATCATCCGCGAGCAAGAACCTGAGCAACAACGC
CTACACCATCATCGTGCACCTGAACGACAGCGTGAGATCGTGTGACCCGCCCAACAACAACACCCGCAAGGGC
ATCCGCATCGGCCCCGGCCAGACCTTCTACGCCACCGAGAATCATCGCGGACATCCGCCAGGCCCACTGCAACA
TCAGCGCCGGCGAGTGAACAAGGCCGTGAGCGCGTGAGCGCCAAGCTGCGCGAGCACTTCCCCAACAAGACCAT
CGAGTTCAGCCCAGCAGCGGGCGGACCTGGAGATCACCACCCACAGCTTCAACTGCCCGGGCGAGTTCTTCTAC
TGCAACACCAGCAAGCTGTTCAACAGCAGCTACAACGGCACCAGCTACCGCGGCACCGAGAGCAACAGCAGCATCA
TCACCCTGCCCTGCCGCATCAAGCAGATCATCGACATGTGGCAGAAGGTGGGCCGCGCCATCTACGCCCCCCCCAT
CGAGGGCAACATCACCTGCAGCAGCAGCATACCGGCCTGCTGCTGGCCCGGACGGCGGCCTGGACAACATCACC
ACCGAGATCTTCCGCCCCAGGGCGGCGACATGAAGGACAACTGGCGCAACGAGCTGTACAAGTACAAGGTGGTGG
AGATCAAGCCCTTGGCGTGCCCCCACCAGGCCAAGCGCCGCGTGGTGGAGCGCGAGAAGCGCGCGCTGGGCAT
CGGGCGCGTGATCTTCGGCTTCTGGGCGCCCGGCAGCAACATGGGCGCCCGCAGCATCACCCTGACCGCCCAG
GCCCCCAGCTGCTGAGCGGCATCGTGCAGCAGCAGAGCAACCTGCTGCGCGCCATCGAGGCCAGCAGCACATGC
TGCAGCTGACCGTGTGGGCATCAAGCAGCTGCAGGCCCGCGTGTGGCCATCGAGCGCTACCTGAAGGACCAGCA
GCTGCTGGGCATCTGGGCTGCAGCGCAAGCTGATCTGCACCACCACCGTGCCCTGGAACAGCAGCTGGAGCAAC
AAGACCCAGGGCGAGATCTGGGAGAACATGACCTGGATGCAGTGGGACAAGGAGATCAGCAACTACACCGGCATCA
TCTACCGCCTGCTGGAGGAGAGCCAGAACCAGCAGGAGCAGAACGAGAAGGACCTGCTGGCCCTGGACAGCGCAA
CAACCTGTGGAGCTGGTTCAACATCAGCAACTGGCTGTGGTACATCAAGATCTTCATCATGATCGTGGCGGCCTG
ATCGGCCTGCGCATCATCTTCGCCGTGCTGAGCATCGTGAACCGCGTGCGCCAGGGCTACAGCCCCCTGAGCTTCC
AGACCCTGACCCCAACCCCGCGGCTGGACCGCTGGGCCGCATCGAGGAGGAGGGCGGCGAGCAGGACCGCGA
CCGAGCATCCGCTGGTGCAGGGCTTCTGGCCCTGGCCTGGGACGACCTGCGCAGCCTGTGCTGTTAGCTAC
CACCGCCTGCGCGACCTGATCCTGGTGACCGCCCGCGTGGTGGAGCTGCTGGGCCGAGCAGCCCCCGCGCCTGC
AGCGCGGTGGGAGGCCCTGAAGTACCTGGGCAGCCTGGTGCAGTACTGGGGCTGGAGCTGAAGAAGAGCGCCAC
CAGCCTGCTGGACAGCATCGCCATCGCCGTGGCCGAGGGCACCGCATCATCGAGGTGATCCAGCGCATCTAC
CGCGCCTTCTGCAACATCCCCCGCGCGTGCGCCAGGGCTTCGAGGCCCGCTGCAGTAA
gp120 (1509) <-- \/--> (1510) gp41
gp140 (2022) <-- \/
gp160, gp41 (2565) <-- \

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ATGGGGGCCCCGCGCCAGCATCCTGCGCGGGCGGCAAGCTGGACGCCTGGGAGCGCATCCGCCTGCGCCCCGG
CGGCAAGAAGTGCTACATGATGAAGCACCTGGTGTGGGGCCAGCCGCGAGCTGGAGAAGTTCGCCCTGAACC
CCGGCCTGTGGAGACCAGCGAGGGCTGCAAGCAGATCATCCGCCAGCTGCACCCCGCCCTGCAGACCGGC
AGCGAGGAGCTGAAGAGCCTGTTCAACACCGTGGCCACCCTGTACTGCGTGCACGAGAAGATCGAGGTGCG
CGACACCAAGGAGGCCCTGGACAAGATCGAGGAGGAGCAGAACAAGTGCCAGCAGAGATCCAGCAGGCCG
AGGCCGCCGACAAGGGCAAGGTGAGCCAGAACTACCCCATCGTGCAGAACCTGCAGGGCCAGATGGTGCAC
CAGGCCATCAGCCCCCGCACCCCTGAACGCCTGGGTGAAGGTGATCGAGGAGAAGGCCTTCAGCCCCGAGGT
GATCCCCATGTTACCGCCCTGAGCGAGGGCGCCACCCCCCAGGACCTGAACACCATGCGTGAACACCGTGG
GCGGCCACCAGGCCGCCATGCAGATGCTGAAGGACACCATCAACGAGGAGGCCCGCGAGTGGGACCGCGTG
CACCCCGTGACGCGCGGCCCATCGCCCCCGGCCAGATGCGCGAGCCCCGCGGCAGCGACATCGCCGGCAC
CACCAGCACCTGCAGGAGCAGATCGOCTGGATGACCAGCAACCCCCCATCCCCGTGGGCGACATCTACA
AGCGCTGGATCATCCTGGGCCTGAACAAGATCGTGCCTATGTACAGCCCCGTGAGCATCCTGGACATCAAG
CAGGGCCCCAAGGAGCCCTTCCGCGACTACGTGGACCGCTTCTTCAAGACCCTGCGCGCCGAGCAGAGCAC
CCAGGAGGTGAAGAACTGGATGACCGACACCCTGCTGGTGCAGAACGCGCAACCCCGACTGCAAGACCATCC
TGCGCGCCCTGGCCCCGGCGCCAGCCTGGAGGAGATGATGACCGCCTGCCAGGGCGTGGGCGGCCCCAGC
CACAAAGGCCCGCGTGTGGCCGAGGCGATGAGCCAGGCCAACACCAGCGTGATGATGCAGAAGAGCAACTT
CAAGGGCCCCCGCGCATCGTGAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCCGCAACTGCCGCG
CCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCACCAGATGAAGGACTGCACCGAGCGGCCAG
GCCAACTTCTGGGCAAGATCTGGCCAGCCACAAGGGCCGCCCGGCAACTTCTGCGAGAGCCGCCCCGA
GCCACCGCCCCCCCCCGCGAGAGCTTCGCTTCGAGGAGACCACCCCGGCCAGAAGCAGGAGAGCAAGG
ACCGCGAGACCCTGACCAGCCTGAAGAGCCTGTTCCGCAACGACCCCTGAGCCAGTAA

Figure 5

Gag_AF110967_BW_opt

ATGGGGCGCCCGCCAGCATCCTGCGCGGCGAGAAGCTGGACAAGTGGGAGAAGATCCGCCTGCGCCCGG
CGGCAAGAAGCACTACATGCTGAAGCACCTGGTGTGGGCCAGCCGCGAGCTGGAGGGGCTTCCCCCTGAACC
CCGGCCTGCTGGAGACCGCCGAGGGCTGCAAGCAGATCATGAAGCAGCTGCAGCCCGCCCTGCAGACCGGC
ACCGAGGAGCTGCGCAGCCTGTACAACACCGTGGCCACCCTGTACTGCGTGCACGCCGCGCATCGAGGTCCG
CGACACCAAGGAGGCCCTGGACAAGATCGAGGAGGAGCAGAACAAGAGCCAGCAGAAGACCCAGCAGGCCA
AGGAGGCCGACGGCAAGGTGAGCCAGAATAACCCATCGTGCAGAACCTGCAGGGCCAGATGGTGCACCAG
GCCATCAGCCCCCGCACCCCTGAACGCCTGGGTGAAGGTGATCGAGGAGAAGGCCTTCAGCCCCGAGGTGAT
CCCCATGTTACCGCCCTGAGCGAGGGCGCCACCCCCAGGACCTGAACACCATGCTGAACACCGTGGGCG
GCCACCAGGCCGCCATGCAGATGCTGAAGGACACCATCAACGAGGAGGCCGCCGAGTGGGACCGCCTGCAC
CCCGTGCAGGCCGGCCCCCGTGGCCCCCGGCCAGATGCGCGACCCCCGCGGCAGCGACATCGCCGGCGCCAC
CAGCAACCCTGCAGGAGCAGATCGCCTGGATGACCAGCAACCCCCCGTGGCCGTGGGCGACATCTACAAGC
CGTGGATCATCCTGGGCCTGAACAAGATCGTGCCTATGTACAGCCCCGTGAGCATCCTGGACATCCGCCAG
GGCCCCAAGGAGCCCTTCCGCGACTACGTGGACCGCTTCTTCAAGACCCCTGCGCGCCGAGCAGGCCACCCA
GGACGTGAAGAACTGGATGACCGAGACCCTGCTGGTGCAGAACGCCAACCCCGACTGCAAGACCATCCTGC
GCGCCCTGGCCCCGGCGCCACCCTGGAGGAGATGATGACCGCCTGCCAGGGCGTGGGCGGCCCGGCCAC
AAGGCCCGCGTGTGGCCGAGGCGATGAGCCAGGCCAACAGCGTGAACATCATGATGCAGAAGAGCAACTT
CAAGGGCCCCCGCGCAACGTCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCAAGAAGTGGCGCG
CCCCCGCAAGAAGGGCTGCTGGAAGTGCAGCAAGGAGGGCCACCAGATGAAGGACTGCACCGAGCGCCAG
GCCAACTTCTGGGCAAGATCTGGCCAGCCACAAGGGCCGCCCGGCAACTTCTGCAGAACCGCAGCGA
GCCCCCGCCCCACCGTGCCACCGCCCCCCCCCGCCGAGAGCTTCCGCTTCGAGGAGACCACCCCGCCC
CCAAGCAGGAGCCCAAGGACCGCGAGCCCTACCGCGAGCCCTGACCGCCCTGCGCAGCCTGTTCCGGCAGC
GGCCCCCTGAGCCAGTAA

Figure 6

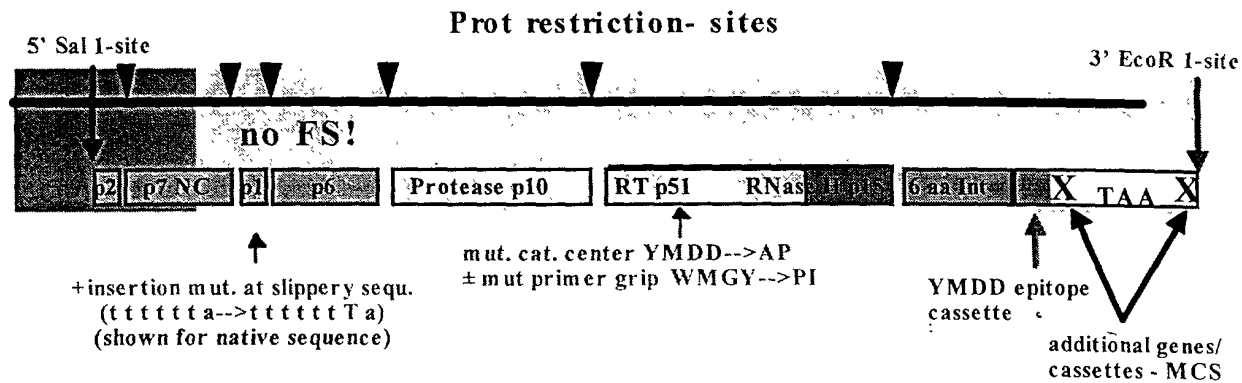


FIGURE 7

PR975(+) (SEQ ID NO:30)

GTCGACGCCACCATGGCCGAGGCCATGAGCCAGGCCACCAGCGCCAACATCCTGAT
GCAGCGCAGCAACTTCAAGGGCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAA
GGAGGGCCACATCGCCCGCAACTGCCGCGCCCCCGCAAGAAGGGCTGCTGGAAGT
GCGGCAAGGAGGGCCACCAGATGAAGGACTGCACCGAGCGCCAGGCCAACTTCTTC
CGCGAGGACCTGGCCTTCCCCCAGGGCAAGGCCCGCGAGTTCCCCAGCGAGCAGAA
CCGCGCCAACAGCCCCACCAGCCGCGAGCTGCAGGTGCGCGGCGACAACCCCCGCA
GCGAGGCCGCGCCGAGCGCCAGGGCACCTGAACTTCCCCAGATCACCTGTGGC
AGCGCCCCCTGGTGAGCATCAAGGTGGGCGGCCAGATCAAGGAGGCCCTGTGGAC
ACCGGCGCCGACGACACCGTGCTGGAGGAGATGAGCCTGCCCGGCAAGTGGAAGCC
CAAGATGATCGGCGGCATCGGCGGCTTCATCAAGGTGCGCCAGTACGACCAGATCCT
GATCGAGATCTGCGGCAAGAAGGCCATCGGCACCGTGCTGATCGGCCCCACCCCCGT
GAACATCATCGGCCGCAACATGCTGACCCAGCTGGGCTGCACCCTGAACTTCCCCAT
CAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCATGGACGGCCCCAAGG
TGAAGCAGTGGCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCGCCATCTGCGAG
GAGATGGAGAAGGAGGGCAAGATCACCAAGATCGGCCCCGAGAACCCCTACAACAC
CCCCGTGTTCGCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGGACT
TCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCC
ACCCCGCCGGCCTGAAGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGGCGACGCC
TACTTCAGCGTGCCCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCC
AGCATCAACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGC
TGGAAGGGCAGCCCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTC
CGCGCCCGCAACCCCCGAGATCGTGATCTACCAGTACATGGACGACCTGTACGTGGGC
AGCGACCTGGAGATCGGCCAGCACCGCGCCAAGATCGAGGAGCTGCGCAAGCACCT
GCTGCGCTGGGGCTTCAACACCCCCGACAAGAAGCACCAAGAGAGCCCCCTTCTCT
GTGGATGGGCTACGAGCTGCACCCCCGACAAGTGGACCGTGACGCCATCGAGCTGCC
CGAGAAGGAGAGCTGGACCGTGAACGACATCCAGAAGCTGGTGGGCAAGCTGAACT
GGGCCAGCCAGATCTACCCCGGCATCAAGGTGCGCCAGCTGTGCAAGCTGCTGCGCG
GCGCCAAGGCCCTGACCGACATCGTGCCCTGACCGAGGAGGCCGAGCTGGAGCTG
GCCGAGAACCGCGAGATCCTGCGCGAGCCCGTGACGGCGTGTACTACGACCCAG
CAAGGACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACCAGTGGACCTACCAGA
TCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAGATGCGCACC
GCCCACACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCATGGA
GAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGAC
CTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTT
CGTGAACACCCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCAT
CGGCGCCGAGACCTTCTACGTGGACGGCGCCGCCAACCGCGAGACCAAGATCGGCA
AGGCCGGCTACGTGACCGACCGGGGCCGCGCAGAAGATCGTGAGCCTGACCGAGACC
ACCAACCAGAAGACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGGCAG
CGAGGTGAACATCGTGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCAGCC
CGACAAGAGCGAGAGCGAGCTGGTGAACCAGATCATCGAGCAGCTGATCAAGAAGG
AGAAGGTGTACCTGAGCTGGGTGCCCGCCACAAGGGCATCGGCGGCAACGAGCAG
ATCGACAAGCTGGTGAGCAAGGGCATCCGCAAGGTGCTGTTCTTGACGGCATCGAT
GGCGGCATCGTGATCTACCAGTACATGGACGACCTGTACGTGGGCAGCGGCGGCCCT
AGGATCGATTAAAAGCTTCCCGGGGCTAGCACCGGTGAATTC

FIGURE 8

PR975YM (SEQ ID NO:31)

GTCGACGCCACCATGGCCGAGGCCATGAGCCAGGCCACCAGCGCCAACATCCTGAT
GCAGCGCAGCAACTTCAAGGGCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAA
GGAGGGCCACATCGCCCGCAACTGCCGCGCCCCCGCAAGAAGGGGTGCTGGAAGT
GCGGCAAGGAGGGGCCACCAGATGAAGGACTGCACCGAGCGCCAGGCCAACTTCTTC
CGCGAGGACCTGGCCTTCCCCCAGGGCAAGGCCCGCGAGTTCCCCAGCGAGCAGAA
CCGCGCCAACAGCCCCACCAGCCGCGAGCTGCAGGTGCGCGGCGACAACCCCCGCA
GCGAGGCCGGCGCCGAGCGCCAGGGCACCTGAACTTCCCCCAGATCACCTGTGGC
AGCGCCCCCTGGTGAGCATCAAGGTGGGCGGCCAGATCAAGGAGGCCCTGCTGGAC
ACCGGCGCCGACGACACCGTGCTGGAGGAGATGAGCCTGCCCGGCAAGTGGAAGCC-
CAAGATGATCGGCGGCATCGGCGGCTTCATCAAGGTGCGCCAGTACGACCAGATCCT
GATCGAGATCTGCGGCAAGAAGGCCATCGGCACCGTGCTGATCGGCCCCACCCCGT
GAACATCATCGGCCGCAACATGCTGACCCAGCTGGGCTGCACCCTGAACTTCCCCAT
CAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCATGGACGGCCCCAAGG
TGAAGCAGTGGCCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCGCCATCTGCGAG
GAGATGGAGAAGGAGGGCAAGATCACCAAGATCGGCCCCGAGAACCCCTACAACAC
CCCCGTGTTTCGCCATCAAGAAGAAGGACAGCACCAAGTGCGCGCAAGCTGGTGGACT
TCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCC
ACCCCGCCGGCCTGAAGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGGCGACGCC
TACTTCAGCGTGCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCC
AGCATCAACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGC
TGGAAGGGCAGCCCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTC
CGCGCCCGCAACCCCGAGATCGTGATCTACCAGGCCCCCTGTACGTGGGCAGCGAC
CTGGAGATCGGCCAGCACCGCGCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCG
CTGGGGCTTACCAACCCCGACAAGAAGCACCAAGGAGCCCCCTTCTGTGGAT
GGGCTACGAGCTGCACCCCGACAAGTGACCGTGACGCCATCGAGCTGCCCGAGA
AGGAGAGCTGGACCGTGAACGACATCCAGAAGCTGGTGGGCAAGCTGAACTGGGCC
AGCCAGATCTACCCCGGCATCAAGGTGCGCCAGCTGTGCAAGCTGCTGCGCGGCGCC
AAGGCCCTGACCGACATCGTGCCCTGACCGAGGAGGCCGAGCTGGAGCTGGCCGA
GAACCGCGAGATCCTGCGCGAGCCCGTGACGGCGTGTACTACGACCCAGCAAGG
ACCTGGTGGCCGAGATCCAGAAGCAGGGCCACGACCAGTGGACCTACCAGATCTAC
CAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAGATGCGCACCGCCCA
CACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCATGGAGAGCA
TCGTGATCTGGGGCAAGACCCCCAAGTTCCGCTGCCATCCAGAAGGAGACCTGGG
AGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTTCGTGA
ACACCCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCATCGGCG
CCGAGACCTTCTACGTGGACGGCGCCGCAACCGCGAGACCAAGATCGGCAAGGCC
GGCTACGTGACCGACCGGGGCGGCAGAAGATCGTGAGCCTGACCGAGACCACCAA
CCAGAAGACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGGCAGCGAGG
TGAACATCGTGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCAGCCCGACA
AGAGCGAGAGCGAGCTGGTGAACCAGATCATCGAGCAGCTGATCAAGAAGGAGAAG
GTGTACCTGAGCTGGGTGCCCGCCACAAGGGCATCGGCGGCAACGAGCAGATCGA
CAAGCTGGTGAAGGGCATCCGCAAGGTGCTGTTCTGGACGGCATCGATGGCG
GCATCGTGATCTACCAGTACATGGACGACCTGTACGTGGGCAGCGGCGGCCCTAGGA
TCGATTAAGGCTTCCCGGGGCTAGCACCGGTGAATTC

FIGURE 9

PR975YMWM (SEQ ID NO:32)

GTCGACGCCACCATGGCCGAGGCCATGAGCCAGGCCACCAGCGCCAACATCCTGAT
GCAGCGCAGCAACTTCAAGGGGCCCCAAGCGCATCATCAAGTGCTTCAACTGCGGCAA
GGAGGGCCACATCGCCCGCAACTGCCGCGCCCCCGCAAGAAGGGCTGCTGGAAGT
GCGGCAAGGAGGGGCCACCAGATGAAGGACTGCACCGAGCGCCAGGCCAACTTCTTC
CGCGAGGACCTGGCCTTCCCCCAGGGCAAGGCCCGCGAGTTCCCCAGCGAGCAGAA
CCGCGCCAACAGCCCCACCAGCCGCGAGCTGCAGGTGCGCGGCGACAACCCCCGCA
GCGAGGCCGGCGCCGAGCGCCAGGGCACCTGAACTTCCCCAGATCACCTGTGGC
AGCGCCCCCTGGTGAGCATCAAGGTGGGCGGCCAGATCAAGGAGGCCCTGCTGGAC-
ACCGGCGCCGACGACACCGTGCTGGAGGAGATGAGCCTGCCCGGCAAGTGGAAGCC
CAAGATGATCGGCGGCATCGGCGGCTTCATCAAGGTGCGCCAGTACGACCAGATCCT
GATCGAGATCTGCGGCAAGAAGGCCATCGGCACCGTGCTGATCGGCCCCACCCCCGT
GAACATCATCGGCCGCAACATGCTGACCCAGCTGGGCTGCACCCTGAACTTCCCCAT
CAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCATGGACGGCCCCAAGG
TGAAGCAGTGGCCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCGCCATCTGCGAG
GAGATGGAGAAGGAGGGCAAGATCACCAAGATCGGCCCCGAGAACCCCTACAACAC
CCCCGTGTTCCGATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGGACT
TCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCC
ACCCCGCCGGCCTGAAGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGGCGACGCC
TACTTCAGCGTGCCCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCC
AGCATCAACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGC
TGGAAGGGCAGCCCCAGCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTC
CGCGCCCCGCAACCCCCGAGATCGTGATCTACCAGGCCCCCCCTGTACGTGGGCAGCGAC
CTGGAGATCGGCCAGCACCGCGCCAAGATCGAGGAGCTGCGCAAGCACCTGCTGCG
CTGGGGCTTCACCACCCCCGACAAGAAGCACCAAGGAGCCCCCTTCCTGCCCAT
CGAGCTGCACCCCCGACAAGTGACCGTGAGCCCATCGAGCTGCCCCGAGAAGGAGA
GCTGGACCGTGAACGACATCCAGAAGCTGGTGGGCAAGCTGAACTGGGCCAGCCAG
ATCTACCCCGGCATCAAGGTGCGCCAGCTGTGCAAGCTGCTGCGCGGCGCCAAGGCC
CTGACCGACATCGTGCCCCCTGACCGAGGAGGCCGAGCTGGAGCTGGCCGAGAACCG
CGAGATCCTGCGCGAGCCCCGTGCACGGCGTGTACTACGACCCAGCAAGGACCTGGT
GGCCGAGATCCAGAAGCAGGGCCACGACCAGTGGACCTACCAGATCTACCAGGAGC
CCTTCAAGAACCTGAAGACCGGCAAGTACGCCAAGATGCGCACCGCCACACCAAC
GACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCATGGAGAGCATCGTGAT
CTGGGGCAAGACCCCCAAGTTCCGCCTGCCCATCCAGAAGGAGACCTGGGAGACCT
GGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTTCGTGAACACCC
CCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGAGCCCATCATCGGCGCCGAG
ACCTTCTACGTGGACGGCGCCGCAACCGCGAGACCAAGATCGGCAAGGCCGGCTA
CGTGACCGACCGGGGGCCGGCAGAAGATCGTGAGCCTGACCGAGACCACCAACCAGA
AGACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGGCAGCGAGGTGAAC
ATCGTGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCAGCCCCGACAAGAG
CGAGAGCGAGCTGGTGAACCAGATCATCGAGCAGCTGATCAAGAAGGAGAAGGTGT
ACCTGAGCTGGGTGCCCCGCCACAAGGGCATCGGCGGCAACGAGCAGATCGACAAG
CTGGTGAGCAAGGGCATCCGCAAGGTGCTGTTCTGGACGGCATCGATGGCGGCATC
GTGATCTACCAGTACATGGACGACCTGTACGTGGGCAGCGGCGGCCCTAGGATCGAT
TAAAGCTTCCCGGGGCTAGCACCGGTGAATTC

FIGURE 10

8_5_ZA (SEQ ID NO:33)

1 TGGAAGGGTT AATTTACTCC AAGAAAAGGC AAGAAATCCT TGATTTGTGG GTCTATCACA
61 CACAAGGCTT CTTCCCTGAT TGGCAAACT ACACACCGGG GCCAGGGGTC AGATATCCAC
121 TGACCTTTGG ATGGTGCTAC AAGCTAGTGC CAGTTGACCC AGGGGAGGTG GAAGAGGCCA
181 ACGGAGGAGA AGACAACGTG TTGCTACACC CTATGAGCCA ACATGGAGCA GAGGATGAAG
241 ATAGAGAAAGT ATTAAGTGG AAGTTTGACA GCCTCCTAGC ACGCAGACAC ATGGCCCGCG
301 AGCTACATCC GGAGTATTAC AAAGACTGCT GACACAGAAG GGACTTTCCG CCTGGGACTT
361 TCCACTGGGG CGTTCCGGGA GGTGTGGTCT GGGCGGGACT TGGGAGTGGT CAACCTCAG
421 ATGCTGCATA TAAGCAGCTG CTTTTCGCCCT GTACTGGGTC TCTCTCGGTA GACCAGATCT
481 GAGCCTGGGA GCCCTCTGGC TATCTAGGGA ACCCACTGCT TAAGCCTCAA TAAAGCTTGC
541 CTTGAGTGCT TTAAGTAGTG TGTGCCCATC TGTTGTGTGA CTCTGGTAAC TAGAGATCCC
601 TCAGACCCTT TGTGGTAGTG TGGAAAATCT CTAGCAGTGG CGCCCGAACA GGGACCAGAA
661 AGTGAAAGTG AGACCAGAGG AGATCTCTCG ACGCAGGACT CGGCTTGCTG AAGTGCACAC
721 GGCAAGAGGC GAGAGGGGCG GCTGGTGAGT ACGCCAATTT TACTTGACTA GCGGAGGCTA
781 GAAGGAGAGA GATGGGTGCG AGAGCGTCAA TATTAAGCGG CGGAAAATTA GATAAATGGG
841 AAAGAATTAG GTTAAGGCCA GGGGGAAGA AACATTATAT GTTAAACAT CTAGTATGGG
901 CAAGCAGGGA GCTGGAAAGA TTTGCACTTA ACCCTGGCCT GTTAGAAACA TCAGAAGGCT
961 GTAAACAAAT AATAAACAG CTACAACCAG CTCTTCAGAC AGGAACAGAG GAACCTTAGAT
1021 CATTATTCAA CACAGTAGCA ACTCTCTATT GTGTACATAA AGGGATAGAG GTACGAGACA
1081 CCAAGGAAGC CTTAGACAAG ATAGAGGAAG AACAAAACAA ATGTCAGCAA AAAGCACAAAC
1141 AGGCAAAAGC AGCTGACGAA AAGGTCAGTC AAAATTATCC TATAGTACAG AATGCCCAAG
1201 GGCAAAATGGT ACACCAAGCT ATATCACCTA GAACATTGAA TGCATGGATA AAAGTAATAG
1261 AGGAAAAGGC TTTCAATCCA GAGGAAATAC CCATGTTTAC AGCATTATCA GAAGGAGCCA
1321 CCCCACAAGA TTTAAACACA ATGTTAAATA CAGTGGGGGG ACATCAAGCA GCCATGCAAA
1381 TGTTAAAAGA TACCATCAAT GAGGAGGCTG CAGAATGGGA TAGGACACAT CCAGTACATG
1441 CAGGGCCTGT TGCACCAGGC CAGATGAGAG AACCAAGGGG AAGTGACATA GCAGGAACTA
1501 CTAGTACCCT TCAGGAACAA ATAGCATGGA TGACAAGTAA TCCACCTATT CCAGTAGAAG
1561 ACATCTATAA AAGATGGATA ATTCTGGGGT TAAATAAAAT AGTAAGAATG TATAGCCCTG
1621 TTAGCATTTT GGACATAAAA CAAGGGCCAA AAGAACCCTT TAGAGACTAT GTAGACCGGT
1681 TCTTTAAAC CTTAAGAGCT GAACAAGCTA CACAAGATGT AAAGAATTGG ATGACAGACA
1741 CCTTGTGGT CCAAATGCG AACCAGATT GTAAGACCAT TTTAAGAGCA TTAGGACCAG
1801 GGGCCTCATT AGAAGAAATG ATGACAGCAT GTCAGGGAGT GGGAGGACCT AGCCATAAAG
1861 CAAGAGTGTT GGCTGAGGCA ATGAGCCAAG CAAACAGTAA CATACTAGTG CAGAGAAGCA
1921 ATTTTAAAGG CTCTAACAGA ATTATTAAAT GTTCAACTG TGGCAAAGTA GGGCACATAG
1981 CCAGAAATTG CAGGGCCCCT AGGAAAAAGG GCTGTTGGAA ATGTGGACAG GAAGGACACC
2041 AAATGAAAGA CTGTACTGAG AGGCAGGCTA ATTTTGTAGG GAAAATTTGG CCTTCCCACA
2101 AGGGGAGGCC AGGGAATTTT CTCCAGAACA GACCAGAGCC AACAGCCCCA CCAGCAGAAC
2161 CAACAGCCCC ACCAGCAGAG AGCTTCAGGT TCGAGGAGAC AACCCCGTG CCGAGGAAGG
2221 AGAAAGAGAG GGAACCTTTA ACTTCCCTCA AATCACTCTT TGGCAGCGAC CCCTTGTCTC
2281 AATAAAAGTA GAGGGCCAGA TAAAGGAGGC TCTCTTAGAC ACAGGAGCAG ATGATACAGT
2341 ATTAGAAGAA ATAGATTTGC CAGGGAATG GAAACCAAAA ATGATAGGGG GAATTGGAGG
2401 TTTTATCAAA GTAAGACAGT ATGATCAAAT ACTTATAGAA ATTTGTGGAA AAAAGGCTAT
2461 AGGTACAGTA TTAGTAGGGC CTACACCAGT CAACATAATT GGAAGAAATC TGTTAACTCA
2521 GCTTGGATGC AACTAAATT TTCCAATTAG TCCTATTGAA ACTGTACCAG TAAATTTAAA
2581 ACCAGGAATG GATGGCCCAA AGGTCAAACA ATGGCCATTG ACAGAAGAAA AAATAAAAGC
2641 ATTAACAGCA ATTTGTGAGG AAATGGAGAA GGAAGGAAAA ATTACAAAAA TTGGGCTTGA
2701 TAATCCATAT AACACTCCAG TATTTGCCAT AAAAAAGAA GACAGTACTA AGTGGAGAAA
2761 ATTAGTAGAT TTCAGGGAAC TCAATAAAG AACTCAAGAC TTTTGGGAAG TTCAATTAGG
2821 AATACCACAC CCAGCAGGAT TAAAAAGAA AAAATCAGTG ACAGTGCTAG ATGTGGGGGA
2881 TGCATATTTT TCAGTTCCTT TAGATGAAAG CTTCAGGAAA TATACTGCAT TCACCATACC

FIGURE 11

2941 TAGTATAAAC AATGAAACAC CAGGGATTAG ATATCAATAT AATGTGCTGC CACAGGGATG
3001 GAAAGGATCA CCAGCAATAT TCCAGAGTAG CATGACAAAA ATCTTAGAGC CCTTCAGAGC
3061 AAAAAATCCA GACATAGTTA TCTATCAATA TATGGATGAC TTGTATGTAG GATCTGACTT
3121 AGAAATAGGG CAACATAGAG CAAAAATAGA AGAGTTAAGG GAACATTTAT TGAAATGGGG
3181 ATTTACAACA CCAGACAAGA AACATCAAAA AGAACCCCA TTTCTTTGGA TGGGGTATGA
3241 ACTCCATCCT GACAAATGGA CAGTACAACC TATACTGCTG CCAGAAAAGG ATAGTTGGAC
3301 TGTCAATGAT ATACAGAAGT TAGTGGGAAA ATTAACTGG GCAAGTCAGA TTTACCCAGG
3361 GATTAAAGTA AGGCAACTCT GTAACTCCT CAGGGGGGCC AAAGCACTAA CAGACATAGT
3421 ACCACTAACT GAAGAAGCAG AATTAGAATT GGCAGAGAAC AGGGAAATTT TAAGAGAACC
3481 AGTACATGGA GTATATTATG ATCCATCAAA AGACTTGATA GCTGAAATAC AGAAACAGGG
3541 GCATGAACAA TGGACATATC AAATTTATCA AGAACCATT AAAAATCTGA AAACAGGGAA
3601 GTATGCAAAA ATGAGGACTA CCCACACTAA TGATGTAAAA CAGTTAACAG AGGCAGTGCA
3661 AAAAAAGACC ATGGAAAGCA TAGTAATATG GGGAAAGACT CCTAAATTTA GACTACCCAT
3721 CCAAAAAGAA ACATGGGAGA CATGGTGGAC AGACTATTGG CAAGCCACCT GGATCCCTGA
3781 GTGGGAGTTT GTTAATACCC CTCCCCTAGT AAAATTATGG TACCAACTAG AAAAAGATCC
3841 CATAGCAGGA GTAGAACTT TCTATGTAGA TGGAGCAACT AATAGGGGAG CTAAATAGG
3901 AAAAGCAGGG TATGTTACTG ACAGAGGAAG GCAGAAAATT GTTACTCTAA CTAACACAAC
3961 AAATCAGAAG ACTGAGTTAC AAGCAATTCA GCTAGCTCTG CAGGATTCTAG GATCAGAAGT
4021 AAACATAGTA ACAGACTCAC AGTATGCATT AGGAATCATT CAAGCACAAC CAGATAAGAG
4081 TGA CTCAGAG ATATTTAACC AAATAATAGA ACAGTTAATA AACAAGGAAA GAATCTACCT
4141 GTCATGGGTA CCAGCACATA AAGGAATTGG GGGAAATGAA CAAGTAGATA AATTAGTAAG
4201 TAAGGGAATT AGGAAAGTGT TGTCTCTAGA TGGAATAGAT AAAGCTCAAG AAGAGCATGA
4261 AAGGTACCAC AGCAATTGGA GAGCAATGGC TAATGAGTTT AATCTGCCAC CCATAGTAGC
4321 AAAAGAAAATA GTAGCTAGCT GTGATAAATG TCAGCTAAAA GGGGAAGCCA TACATGGACA
4381 AGTCGACTGT AGTCCAGGGA TATGGCAATT AGATTGTACC CATTTAGAGG GAAAAATCAT
4441 CCTGGTAGCA GTCCATGTAG CTAGTGGCTA CATGGAAGCA GAGGTTATCC CAGCAGAAAC
4501 AGGACAAGAA ACAGCATATT TTATATTTAA ATTAGCAGGA AGATGGCCAG TCAAAGTAAT
4561 ACATACAGAC AATGGCAGTA ATTTTACCAG TACTGCAGTT AAGGCAGCCT GTTGGTGGGC
4621 AGGTATCCAA CAGGAATTTG GAATTCCTTA CAATCCCCAA AGTCAGGGAG TGGTAGAATC
4681 CATGAATAAA GAATTAAAGA AAATAATAGG ACAAGTAAGA GATCAAGCTG AGCACCTTAA
4741 GACAGCAGTA CAAATGGCAG TATTCATTCA CAATTTTAAA AGAAAAGGGG GAATTGGGGG
4801 GTACAGTGCA GGGGAAAGAA TAATAGACAT AATAGCAACA GACATACAAA CTAAAGAATT
4861 ACAAAAACAA ATTATAAGAA TTCAAAATTT TCGGGTTTAT TACAGAGACA GCAGAGACCC
4921 TATTTGGAAA GGACCAGCCG AACTACTCTG GAAAGGTGAA GGGGTAGTAG TAATAGAAGA
4981 TAAAGGTGAC ATAAAGGTAG TACCAAGGAG GAAAGCAAAA ATCATTAGAG ATTATGGAAA
5041 ACAGATGGCA GGTGCTGATT GTGTGGCAGG TGGACAGGAT GAAGATTAGA GCATGGAATA
5101 GTTTAGTAAA GCACCATATG TATATATCAA GGAGAGCTAG TGGATGGGTC TACAGACATC
5161 ATTTTGAAAG CAGACATCCA AAAGTAAGTT CAGAAGTACA TATCCCATTA GGGGATGCTA
5221 GATTAGTAAT AAAAACATAT TGGGGTTTGC AGACAGGAGA AAGAGATTGG CATTTGGGTC
5281 ATGGAGTCTC CATAGAATGG AGACTGAGAG AATACAGCAC ACAAGTAGAC CCTGACCTGG
5341 CAGACCAGCT AATTCACATG CATTATTTTG ATTGTTTTAC AGAATCTGCC ATAAAGACAAG
5401 CCATATTAGG ACACATAGTT TTTCTAGGT GTGACTATCA AGCAGGACAT AAGAAGGTAG
5461 GATCTCTGCA ATACTTGGCA CTGACAGCAT TGATAAAACC AAAAAAGAGA AAGCCACCTC
5521 TGCCTAGTGT TAGAAAATTA GTAGAGGATA GATGGAACGA CCCCAGAAG ACCAGGGGCC
5581 GCAGAGGGAA CCATACAATG AATGGACACT AGAGATTCTA GAAGAACTCA AGCAGGAAGC
5641 TGTCAGACAC TTTCTAGAC CATGGCTCCA TAGCTTAGGA CAATATATCT ATGAAACCTA
5701 TGGGGATACT TGGACGGGAG TTGAAGCTAT AATAAGAGTA CTGCAACAAC TACTGTTTCAT
5761 TCATTTTACA ATTGGATGCC AACATAGCAG AATAGGCATC TTGCGACAGA GAAGAGCAAG
5821 AAATGGAGCC AGTAGATCCT AAATAAAGC CCTGGAACCA TCCAGGAAGC CAACCTAAAA
5881 CAGCTTGTA TAATTGCTTT TGCAAACT GTAGCTATCA TTGTCTAGTT TGCTTTTACA

FIGURE 11

5941 CAAAAGGTTT AGGCATTTCC TATGGCAGGA AGAAGCGGAG ACAGCGACGA AGCGCTCCTC
6001 CAAGTGGTGA AGATCATCAA AATCCTCTAT CAAAGCAGTA AGTACACATA GTAGATGTAA
6061 TGGTAAGTTT AAGTTTATTT AAAGGAGTAG ATTATAGATT AGGAGTAGGA GCATTGATAG
6121 TAGCACTAAT CATAGCAATA ATAGTGTGGA CCATAGCATA TATAGAATAT AGGAAATTGG
6181 TAAGACAAAA GAAAATAGAC TGGTTAATTA AAAGAATTAG GGAAAGAGCA GAAGACAGTG
6241 GCAATGAGAG TGATGGGGAC ACAGAAGAAT TGTCAACAAT GGTGGATATG GGGCATCTTA
6301 GGCTTCTGGA TGCTAATGAT TTGTAACACG GAGGACTTGT GGGTCACAGT CTACTATGGG
6361 GTACCTGTGT GGAGAGAAGC AAAAATACT CTATTCTGTG CATCAGATGC TAAAGCATAT
6421 GAGACAGAAG TGCATAATGT CTGGGCTACA CATGCTTGTG TACCCACAGA CCCCAACCCA
6481 CAAGAAATAG TTTTGGGAAA TGTAACAGAA AATTTTAATA TGTGGAAAAA TAACATGGCA
6541 GATCAGATGC ATGAGGATAT AATCAGTTTA TGGGATCAAA GCCTAAAGCC ATGTGTAAAG
6601 TTGACCCAC TCTGTGTCAC TTTAACTGT ACAGATACAA ATGTTACAGG TAATAGAACT
6661 GTTACAGGTA ATACAAATGA TACCAATATT GCAAATGCTA CATATAAGTA TGAAGAAATG
6721 AAAAATTGCT CTTTCAATGC AACCACAGAA TTAAGAGATA AGAAACATAA AGAGTATGCA
6781 CTCTTTTATA AACTTGATAT AGTACCACTT AATGAAAATA GTAACAACTT TACATATAGA
6841 TTAATAAATT GCAATACCTC AACCATAACA CAAGCCTGTC CAAAGGTCTC TTTTGACCCG
6901 ATTCTTATAC ATTACTGTGC TCCAGCTGAT TATGCGATTG TAAAGTGTA TAATAAGACA
6961 TTCAATGGGA CAGGACCATG TTATAATGTC AGCACAGTAC AATGTACACA TGGAATTAAAG
7021 CCAGTGGTAT CAACTCAACT ACTGTAAAT GGTAGTCTAG CAGAAGAAGG GATAATAATT
7081 AGATCTGAAA ATTTGACAGA GAATACCAA ACAATAATAG TACATCTTAA TGAATCTGTA
7141 GAGATTAATT GTACAAGGCC CAACAATAAT ACAAGGAAAA GTGTAAGGAT AGGACCAGGA
7201 CAAGCATTTCT ATGCAACAAA TGACGTAATA GGAAACATAA GACAAGCACA TTGTAACATT
7261 AGTACAGATA GATGGAATAA AACTTTACAA CAGGTAATGA AAAAATTAGG AGAGCATTTT
7321 CCTAATAAAA CAATAAAATT TGAACCACAT GCAGGAGGGG ATCTAGAAAT TACAATGCAT
7381 AGCTTTAATT GTAGAGGAGA ATTTTCTAT TGCAATACAT CAAACCTGTT TAATAGTACA
7441 TACTACCTTA AGAATGGTAC ATACAAATAC AATGGTAATT CAAGCTTACC CATCACACTC
7501 CAATGCAAAA TAAACAAAT TGTACGCATG TGGCAAGGGG TAGGACAAGC AATGTATGCC
7561 CCTCCCATTG CAGGAAACAT AACATGTAGA TCAAACATCA CAGGAATACT ATTGACACGT
7621 GATGGGGGAT TTAACAACAC AAACAACGAC ACAGAGGAGA CATTAGACC TGGAGGAGGA
7681 GATATGAGGG ATAAGTGGAG AAGTGAATTA TATAAATATA AAGTGGTAGA AATTAAGCCA
7741 TTGGGAATAG CACCCACTAA GGCAAAAAGA AGAGTGGTGC AGAGAAAAAA AAGAGCAGTG
7801 GGAATAGGAG CTGTGTTCTT TGGGTTCTTG GGAGCAGCAG GAAGCACTAT GGGCGCAGCG
7861 TCAATAACGC TGACGGTACA GGCCAGACAA CTGTTGTCTG GTATAGTGCA ACAGCAAAGC
7921 AATTTGCTGA AGGCTATAGA GCGCAACAG CATATGTTGC AACTCACAGT CTGGGGCATT
7981 AAGCAGCTCC AGGCGAGAGT CCTGGCTATA GAAAGATACC TAAAGGATCA ACAGCTCCTA
8041 GGGATTTGGG GCTGCTCTGG AAGACTCATC TGCACCACTG CTGTGCCTTG GAACTCCAGT
8101 TGGAGTAATA AATCTGAAGC AGATATTTGG GATAACATGA CTTGGATGCA GTGGGATAGA
8161 GAAATTAATA ATTACACAGA AACAAATATC AGGTGCTTG AAGACTCGCA AAACCAGCAG
8221 GAAAAGAATG AAAAAGATTT ATTAGAATTG GACAAGTGGA ATAATCTGTG GAATTGGTTT
8281 GACATATCAA ACTGGCTGTG GTATATAAAA ATATTCATAA TGATAGTAGG AGGCTTGATA
8341 GGTTTAAGAA TAATTTTGC TGTGCTCTCT ATAGTGAATA GAGTTAGGCA GGGATACTCA
8401 CCTTTGTCAT TTCAGACCCT TACCCCAAGC CCGAGGGGAC TCGACAGGCT CGGAGGAATC
8461 GAAGAAGAAG GTGGAGAGCA AGACAGAGAC AGATCCATAC GATTGGTGAG CGGATTCTTG
8521 TCGCTTGCCCT GGGACGATCT GCGGAGCCTG TGCTCTTCA GCTACCACCG CTTGAGAGAC
8581 TTCATATTAA TTGCAGTGAG GGCAGTGGA CTTCTGGGAC ACAGCAGTCT CAGGGGACTA
8641 CAGAGGGGGT GGGAGATCCT TAAGTATCTG GGAAGTCTTG TGCAGTATTG GGGTCTAGAG
8701 CTAAAAAAGA GTGCTATTAG TCCGCTTGAT ACCATAGCAA TAGCAGTAGC TGAAGGAACA
8761 GATAGGATTA TAGAATTGGT ACAAAGAATT TGTAAGAGCTA TCCTCAACAT ACCTAGGAGA
8821 ATAAGACAGG GCTTTGAAGC AGCTTTGCTA TAAATGGGA GGCAAGTGGT CAAAACGCAG
8881 CATAGTTGGA TGGCCTGCAG TAAGAGAAAG AATGAGAAGA ACTGAGCCAG CAGCAGAGGG
8941 AGTAGGAGCA GCGTCTCAAG ACTTAGATAG ACATGGGGCA CTTACAAGCA GCAACACACC

FIGURE 11

9001	TGCTACTAAT	GAAGCTTGTG	CCTGGCTGCA	AGCACAAAGAG	GAGGACGGAG	ATGTAGGCTT
9061	TCCAGTCAGA	CCTCAGGTAC	CTTTAAGACC	AATGACTTAT	AAGAGTGCAG	TAGATCTCAG
9121	CTTCTTTTTA	AAAGAAAAGG	GGGGACTGGA	AGGGTTAATT	TACTCTAGGA	AAAGGCAAGA
9181	AATCCTTGAT	TTGTGGGTCT	ATAACACACA	AGGCTTCTTC	CCTGATTGGC	AAAACACAC
9241	ATCGGGGCCA	GGGGTCCGAT	TCCCAC TGAC	CTTTGGATGG	TGCTTCAAGC	TAGTACCAGT
9301	TGACCCAAGG	GAGGTGAAAG	AGGCCAATGA	AGGAGAAGAC	AACTGTTTGC	TACACCCTAT
9361	GAGCCAACAT	GGAGCAGAGG	ATGAAGATAG	AGAAGTATTA	AAGTGGAAGT	TTGACAGCCT
9421	TCTAGCACAC	AGACACATGG	CCCGCGAGCT	ACATCCGGAG	TATTACAAAG	ACTGCTGACA
9481	CAGAAGGGAC	TTTCCGCCTG	GGACTTTCCA	CTGGGGCGTT	CCGGGAGGTG	TGGTCTGGGC
9541	GGGACTTGGG	AGTGGTCACC	CTCAGATGCT	GCATATAAGC	AGCTGCTTTT	CGCTTG TACT
9601	GGGTCTCTCT	CGGTAGACCA	GATCTGAGCC	TGGGAGCTCT	CTGGCTATCT	AGGGAACCCA
9661	CTGCTTAGGC	CTCAATAAAG	CTTGCC TTGA	GTGCTCTAAG	TAGTGTGTGC	CCATCTGTTG
9721	TGTGACTCTG	GTAAC TAGAG	ATCCCTCAGA	CCCTTTGTGG	TAGTGTGGAA	AATCTCTAGC
9781	A					

FIGURE 11

SEQ ID NO:34

GCTGAGGCAATGAGCCAAGCAACCAGCGCAAACATACTGATGCAGAGAAGCAATTT
CAAAGGCCCTAAAAGAATTATTAAATGTTTCAACTGTGGCAAGGAAGGGCACATAG
CTAGAAATTGTAGGGCCCCTAGGAAAAAAGGCTGTTGGAAATGTGGAAAGGAAGGA
CACCAAATGAAAGACTGTACTGAGAGGCAGGCTAA

FIGURE 12

FIGURE 12

975Pol wt until 6aa Int: (SEQ ID NO:35)

TTTTTTAGGGAAGATTTGGCCTTCCCAACAAGGGAAGGCCAGGGAATTTTCCTTCAGAA
CAGAACAGAGCCAACAGCCCCACCAGCAGAGAGCTTCAAGTTCGAGGAGACAACCC
CCGCTCCGAAGCAGGAGCCGAAAGACAGGGAACCCCTTAATTTCCCTCAAATCACTCT
TTGGCAGCGACCCCTTGTCTCAATAAAAGTAGGGGGTCAAATAAAGGAGGCTCTCTT
AGACACAGGAGCTGATGATACAGTATTAGAAGAAATGAGTTTGCCAGGAAAATGGA
AACCAAAAATGATAGGAGGAATTGGAGGTTTTATCAAAGTAAGACAGTATGATCAA
ATACTTATAGAAATTTGTGGAAAAAAGGCTATAGGTACAGTATTAATAGGACCTACA
CCTGTCAACATAATTGGAAGGAATATGTTGACTCAGCTTGGATGCACACTAAATTTT
CCAATTAGTCCCATTGAACTGTGCCAGTAAAAATTAAAGCCAGGAATGGATGGCCCA
AAGGTTAAACAATGGCCATTGACAGAAGAGAAAAATAAAAGCATTAAACAGCAATTTG
TGAAGAAATGGAGAAAAGAAGGAAAAATTACAAAAATTGGGCCTGAAAATCCATATA
ACACTCCAGTATTTGCCATAAAAAAGAAGGACAGTACTAAGTGGAGAAAAGTTAGTA
GATTTTCAGGGAACCTTAATAAAAGAACTCAAGACTTTTGGGAAGTTCAATTAGGAATA
CCACACCCAGCAGGGTTAAAAAAGAAAAAATCAGTGACAGTACTGGATGTGGGGGA
TGCATATTTTTTCAGTTCCCTTTAGATGAGGACTTCAGGAAATATACTGCATTCACCATA
CCTAGTATAAAACAATGAAACACCAGGGATTAGATATCAATATAATGTGCTTCCACAG
GGATGGAAAGGATCACCATCAATATTCCAGAGTAGCATGACAAAAATCTTAGAGCC
CTTTAGAGCAAGAAATCCAGAAATAGTCATCTATCAATATATGGATGACTTGTATGT
AGGATCTGACTTAGAAATAGGGCAACATAGAGCAAAAAATAGAGGAGTTAAGAAAAC
ATCTGTAAAGGTGGGGATTTACCACACCGGACAAGAAACATCAGAAAGAACCCCCA
TTTCTTTGGATGGGGTATGAACTCCATCCTGACAAATGGACAGTACAGCCTATAGAG
TTGCCAGAAAAGGAAAGCTGGACTGTCAATGATATACAGAAGTTAGTGGGAAAATT
AAATTGGGCCAGTCAGATTTACCCAGGAATTAAAGTAAGGCAACTTTGTAACTCCT
TAGGGGGGCCAAAGCACTAACAGATATAGTACCACTAACTGAAGAAGCAGAATTAG
AATTGGCAGAGAACAGGGAAATTCTAAGAGAACCAGTACATGGAGTATATTATGAC
CCATCAAAAGACTTGGTAGCTGAAATACAGAAACAGGGGCATGACCAATGGACATA
TCAATTTACCAAGAACCATTCAAAAACCTGAAAACAGGGAAGTATGCAAAAATGA
GGACTGCCCACTAATGATGTAAAAACAGTTAACAGAGGCAGTGCAAAAAATAGCT
ATGGAAAGCATAGTAATATGGGGAAAGACTCCTAAATTTAGACTACCCATCCAAAA
AGAAACATGGGAGACATGGTGGACAGACTATTGGCAAGCCACCTGGATTCTGAGT
GGGAGTTTGTTAATACCCCTCCCTTAGTAAAATTATGGTACCAGCTAGAGAAAGAAC
CCATAATAGGAGCAGAACTTTCTATGTAGATGGAGCAGCTAATAGGGAAACTAAA
ATAGGAAAAGCAGGGTATGTTACTGACAGAGGAAGGCAGAAAATTGTTTCTCTAAC
AGAAACAACAAATCAGAAGACTGAATTACAAGCAATTCAGCTAGCTTTGCAAGATT
AGGATCAGAAGTAAACATAGTAACAGACTCACAGTATGCATTAGGAATCATTCAAG
CACAACCAGATAAGAGTGAATCAGAGTTAGTCAACCAAATAATAGAACAATTAATA
AAAAAGGAAAAGGTCTACCTGTCATGGGTACCAGCACATAAAGGAATTGGAGGAAA
TGAACAAATAGATAAATTAGTAAGTAAGGGAATCAGGAAAGTGCTGTTTCTAGATG
GAATAGAT

FIGURE 13

SEQ ID NO:36

GGCGGCATCGTGATCTACCAGTACATGGACGACCTGTACGTGGGCAGCGGCG
GC

FIGURE 14

FIGURE 14

SEQ ID NO: 37

GGIVTYQYMDDLTVGSGG

FIGURE 15

105040336060

12_5/1ZA (SEQ ID NO:45)

TGGAAGGGTTAATTTACTCCAGGAAAAGGCAAGAGATCCTTGATTTATGGGTCTATC
ACACACAAGGCTACTTCCCTGATTGGCAAACTACACACCGGGACCAGGGGTCAGA
TATCCACTGACCTTTGGATGGTGCTTCAAGCTAGTGCCAGTTGACCCAAGGGAAGTA
GAAGAGGCCAACGGAGGAGAAGACAACCTGTTTGCTACACCCTATGAGCCAGTATGG
AATGGATGATGAACACAAAGAAGTGTTACAGTGGAAGTTTGACAGCAGCCTAGCAC
GCAGACACCTGGCCCGCGAGCTACATCCGGATTATTACAAAGACTGCTGAÇACAGA
AGGGACTTTCCGCCTGGGACTTTCCACTGGGGCGTTCCAGGGGGAGTGGTCTGGGCG
GGACTGGGAGTGGCCAGCCCTCAGATGCTGCATATAAGCAGCGGCTTTTCGCCTGTA
CTGGGTCTCTCTAGGTAGACCAGATCCGAGCCTGGGAGCTCTCTGTCTATCTGGGGA
ACCCACTGCTTAGGCCTCAATAAAGCTTGCTTGAGTGCTCTAAGTAGTGTGTGCCC
ATCTGTTGTGTGACTCTGGTAACTCTGGTAACTAGAGATCCCTCAGACCCTTTGTGGT
AGTGTGGAATACTCTAGCAGTGGCGCCCCGAACAGGGACTTGAAAGCGAAAGTGAG
ACCAGAGAAGATCTCTCGACGCAGGACTCGGCTTGCTGAAGTGCACTCGGCAAGAG
GCGAGGGGGGCGACTGGTGAGTACGCCAAAATTTTTTTTACTAGCGGAGGCTAGA
AGGAGAGAGATGGGTGCGAGAGCGTCAATATTAAGAGGGGGGAAAATTAGACAAAT
GGGAAAAAATTAGGTTACGGCCAGGGGGGAGAAAACACTATATGCTAAAACACCTA
GTATGGGCAAGCAGAGAGCTGGAAAGATTTGCAGTTAACCCTGGCCTTTTAGAGAC
ATCAGACGGATGTAGAC AAATAATAAAACAGCTACAACCAGCTCTTCAGA
CAGGAACAGAGGAAATTAGATCATTATTTAACACAGTAGCAACTCTCTATTGTGTAC
ATAAAGGGATAGATGTACGAGACACCAAGGAAGCCTTAGACAAGATAGAGGAGGA
ACAAAACAAATGTCAGCAAAAAACACAGCAGGCGGAAGCGGCTGACAAAAAGGTC
AGTCAAAATTATCCTATAGTGCAGAACCTCCAAGGGCAAATGGTACACCAGGCCAT
ATCACCTAGAACCCTGAATGCATGGGTAAAAGTAATAGAGGAGAAGGCTTTTAGCC
CAGAGGTAATACCCATGTTTACAGCATTATCAGAAGGAGCCACCCACAAGATTTA
AACACCATGTAAATACAGTGGGGGGACATCAAGCAGCCATGCAAATGTAAAAG
ATACCATCAATGAGGAGGCTGCAGAATGGGATAGGTTACATCCAGTACATGCAGGG
CCTGTTGCACCAGGCCAGATGAGAGAACCAAGGGGAAGTGACATAGCAGGAACTA
CTAGTACCCTTCAAGAACAAATAGCATGGATGACAAGTAACCCACCTATCCCAGTA
GGGGACATCTATAAAAGGTGGATAATTCTGGGGTTAAATAAAATAGTAAGAATGTA
CAGCCCTGTCAGCATTTTAGACATAAAACAAGGACCAAAGGAACCCTTTAGAGACT
ATGTAGACCGGTTCTTCAAACTTTAAGAGCTGAACAATCTACACAAGAGGTAAAA
AATTGGATGACAGACACCTTGTTAGTCCAAAATGCGAACCAGATTGTAAGACCATT
TTAAGAGCATTAGGACCAGGGGCTTCATTAGAAGAAATGATGACAGCATGTCAGGG
AGTGGGAGGACCTAGCCACAAAGCAAGAGTTTTGGCTGAGGCAATGAGCCAAGCAA
ACAATACAAGTGTAATGATACAGAAAAGCAATTTTAAAGGCCCTAGAAGAGCTGTT
AAATGTTTCAACTGTGGCAGGGAAGGGCACATAGCCAGGAATTGCAGGGCCCCTAG
GAAAAGGGGCTGTTGGAAATGTGGAAAGGAAGGACACCAAATGAAAGACTGTACT
GAGAGGCAGGCTAATTTTTTAGGGAAAATTTGGCCTTCCCACAAGGGGAGGCCAGG
GAATTTCCCTTCAGAGCAGACCAGAGCCAACAGCCCCACCACTAGAACCAACAGCCC
CACCAGCAGAGAGCTTCAAGTTCAAGGAGACTCCGAAGCAGGAGCCGAAAGACAG
GGAACCTTTAACTTCCCTCAAATCACTCTTTGGCAGCGACCCCTTGTCTCAATAAAA

FIGURE 16

GTAGCGGGCCAAACAAAGGAGGCTCTTTTAGATACAGGAGCAGATGATACAGTACT
 AGAAGAAATAAACTTGCCAGGAAAATGGAAACCAAAAATGATAGGAGGAATTGGA
 GGTTTTATCAAAGTAAGACAGTATGATCAAATACTTATAGAAATTTGTGGAAAAAGG
 GCTATAGGTACAGTATTAGTAGGACCTACACCTGTCAACATAATTGGAAGAAATCTG
 TTGACTCAGCTTGGATGCACACTAAATTTTCCAATTAGCCCCATTGAACTGTACCA
 GTAAAATTAAAGCCAGGAATGGATGGCCCAAAGGTAAACAATGGCCATTGACAGA
 AGAAAAAATAAAAGCATTAAACAGAAATTTGTGAGGAAATGGAGAAGGAAGGAAAA
 ATTACAAAAATTGGGCCTGAAAATCCATATAACACTCCAGTATTTGCCATAAAGAAG
 AAGGACAGTACAAAGTGGAGAAAATTAGTAGATTTTCAGGGAACTCAATAAAAGAAC
 TCAAGACTTTTGGGAAGTCCAATTAGGAATACCACACCCAGCAGGGTTAAAAAAGA
 AAAAATCAGTGACAGTACTGGATGTGGGAGATGCATATTTTTTCAGTCCCTTTAGATG
 AGAGCTTCAGAAAATATACTGCATTACCATACCTAGTATAAACAATGAAACACCA
 GGGATTAGATATCAATATAATGTTCTTCCACAGGGATGGAAAGGATCACCAGCAA
 TATTCCAGAGTAGCATGACAAGAATCTTAGAGCCCTTTAGAACACAAAACCCAGAA
 GTAGTTATCTATCAATATATGGATGACTTATATGTAGGATCTGACTTAGAAATAGGG
 CAACATAGAGCAAAAATAGAGGAGTTAAGAGGACACCTATTGAAATGGGGATTTAC
 CACACCAGACAAGAAACATCAGAAAGAACCCCCATTTCTTTGGATGGGGTATGAAC
 TCCATCCTGACAAATGGACAGTACAGCCTATACAGCTGCCAGAAAAGGAGAGCTGG
 ACTGTCAATGATATACAGAAAGTTAGTGGGAAAGTTAAACTGGGCAAGTCAGATTTA
 CCCAGGGATTAAAGTAAGGCAACTGTGTAAACTCCTTAGGGGAGCCAAAGCACTAA
 CAGACATAGTGCCACTGACTGAAGAAGCAGAATTAGAATTGGCTGAGAACAGGGA
 AATTCTAAAAGAACAGTACATGGAGTATATTATGACCCATCAAAAAGATTTAATAG
 CTGAAATACAGAAACAGGGGAATGACCAATGGACATATCAAATTTACCAAGAACC
 ATTTAAAAATCTGAGAACAGGAAAGTATGCAAAAATGAGGACTGCCCACACTAATG
 ATGTGAAACAGTTAGCAGAGGCAGTGCAAAAGATAACCCAGGAAAGCATAGTAATA
 TGGGGAAAAACTCCTAAATTTAGACTACCCATCCCAAAAAGAAACATGGGAGACATG
 GTGGTCAGACTATTGGCAAGCCACCTGGATTCTGAGTGGGAGTTTGTCAATACCCC
 TCCCCTAGTAAAATTGTGGTACCAGCTGGAAAAAGAACCCATAGTAGGGGCAGAAA
 CTTTCTATGTAGATGGAGCAGCCAATAGGGAAACTAAAATAGGAAAAGCAGGGTAT
 GTCACTGACAAAGGAAGGCAGAAAGTTGTTTCCTTCACTGAAACAACAAATCAGAA
 GACTGAATTACAAGCAATTCAGCTAGCTTTGCAGGATTCAGGGCCAGAAGTAAACA
 TAGTAACAGACTCACAGTATGCATTAGGAATCATTCAAGCACAACCAGATAAGAGT
 GAATCAGAATTAGTCAGTCAAATAATAGAACAGTTGATAAAAAAGGAAAAAGTCTA
 CCTATCATGGGTACCAGCACATAAAGGAATTGGAGGAAATGAACAAGTAGACAAAT
 TAGTAAGTAGTGGAATCAGAAAAGTACTGTTTCTAGATGGAATAGATAAAGCTCAA
 GAAGAGCATGAAAAATATCACAGCAATTGGAGAGCAATGGCTAGTGAGTTTAATCT
 GCCACCCATAGTAGCAAAGGAAATAGTAGCCAGCTGTGATAAATGTCAGCTAAAAG
 GGAAGCCATGCATGGACAAGTCGACTGTAGTCCAGGAATATGGCAATTAGACTGT
 ACACATTTAGAAGGAAAAATCATCCTAGTAGCAGTCCATGTAGCCAGTGGCTACAT
 GGAAGCAGAGGTTATCCAGCAGAAACAGGACAAGAAACAGCATACTTTATACTAA
 AATTAGCAGGAAGATGGCCAGTCAAAGTAATACATACAGATAATGGCAGTAATTTT
 ACCAGTACCGCAGTTAAGGCAGCCTGTTGGTGGGCAGATATCCAACGGGAATTTGG
 AATCCCTACAATCCCCAAAGTCAAGGAGTAGTAGAATCCATGAATAAAGAATTAA

FIGURE 16

AGAAAATCATAGGGCAAGTAAGAGATCAAGCTGAGCACCTTAAGACAGCAGTACAA
ATGGCAGTATTCATTACAAATTTTAAAAGAAAAGGGGGGATTGGGGGGTACAGTGC
AGGGGAGAGAATAATAGACATAATAGCATCAGACATACAACTAAAGAATTACAAA
AACAAATTATAAAAATTCAAATTTTCGGGTTTATTACAGAGACAGCAGAGACCCTA
TTTGGAAGAGACCAGCCAACTACTCTGGAAAGGTGAAGGGGCAGTAGTAATACAA
GATAATAGTGATATAAAGGTAGTACCAAGAAGGAAAAGCAAAAATCATTAAAGGACTA
TGGAAAACAGATGGCAGGTGCTGATTGTGTGGCAGGTAGACAGGATGAAGATTAGA
ACATGGCACAGTTTAGTAAAGCACCATATGTATGTTTCGAGGAGAGCTGATGGATGG
TTCTACAGACATCATTATGAAAGCAGACACCCAAAAGTAAGTTCAGAAGTACACAT
CCCATTAGGAGATGCCAGGTAGTAATAAAAACATATTGGGGTCTGCAGACAGGAG
AAAGAGCTTGGCATTGTTGGGTCACGGAGTCTCCATAGAATGGAGATTGAGAAGATAT
AGCACACAAGTAGACCCTGACCTGACAGACCACTAATTCATATGCATTATTTTGAT
TGTTTTGCAGAATCTGCCATAAGGAAAGCCATACTAGGACAGATAGTTAGCCCTAA
GTGTGACTATCAAGCAGGACATAACAAGGTAGGATCTCTACAATACTTGGCACTGA
CAGCATTGATAAAACCAAAAAAGATAAAGCCACCTCTGCCTAGTGTTAGGAAATTA
GTAGAGGATAGATGGAACAAGCCCCAGAAGACCAGGGGCCGAGAGGGAACCATA
CAATGAATGGACACTAGAGCTTTTAGAAGAACTCAAGCAGGAAGCTGTCAGACACT
TTCCTAGACCATGGCTCCATAACTTAGGACAACATATCTATGAAACCTATGGAGATA
CTTGACAGGAGTTGAAGCAATAATAAGAATCCTGCAACAATTACTGTTTATTATT
TCAGGATTGGGTGCCATCATAGCAGAATAGGCATTTTGCGACAGAGAAGAGCAAGA
AATGGAGCCAATAGATCCTAACCTAGAACCCTGGAACCATCCAGGAAGTCAGCCTA
AACTGCTTGTAATGGGTGTTACTGTAAACGTTGCAGCTATCATTGTCTAGTTTGCTT
TCAGAAAAAAGGCTTAGGCATTTACTATGGCAGGAAGAAGCGGAGACAGCGACGAA
GCGCTCCTCCAAGCAATAAAGATCATCAAGATCCTCTACCAAAGCAGTAAGTACCG
AATAGTATATGTAATGTTAGATTAACTGCAAGAATAGATTCTAGATTAGGAATAGG
AGCATTGATAGTAGCACTAATCATAGCAATAATAGTGTGGACCATAGTATATATAG
AATATAGGAAATTGGTAAGGCAAAGGAAAATAGACTGGTTAGTTAAAAGGATTAGG
GAAAGAGCAGAAGACAGTGGCAATGAGAGCGAGGGGGATACTGAAGAATTATCGA
CACTGGTGGATATGGGGCATCTTAGGCTTTTGGATGCTAATGATGTGTAATGTGAA
GGGCTTGTGGGTCACAGTCTACTACGGGGTACCTGTGGGGAGAGAAGCAAAAAT
ACTCTATTTTGTGCATCAGATGCTAAAGCATATGAGAAAGAAGTGCATAATGTCTG
GGCTACACATGCCTGTGTACCCACAGACCCCAACCCACAAGAAGTGATTTTGGGC
AATGTAACAGAAAAATTTTAACATGTGGAATAATGACATGGTGGATCAGATGCAGG
AAGATATAATCAGTTTATGGGATCAAAGCCTTAAGCCATGTGTAAAATTGACCCCA
CTCTGTGTCACTTTAACTGTACAAATGCAACTGTAACTACAATAATACCTCTAAA
GACATGAAAAATTGCTCTTTCTATGTAACCACAGAATTAAGAGATAAGAAAAAGAA
AGAAAATGCACTTTTTTATAGACTTGATATAGTACCACTTAATAATAGGAAGAATGG
GAATATTAACAACCTATAGATTAATAAATTGTAATACCTCAGCCATAACACAAGCCTG
TCCAAAAGTCTCGTTTGACCCAATTCCTATACATTATTGTGCTCCAGCTGGTTATGCG
CCTCTAAAATGTAATAATAAGAAATTCAATGGAATAGGACCATGCGATAATGTCAG
CACAGTACAATGTACACATGGAATTAAGCCAGTGGTATCAACTCAATTACTGTTAAA
TGGTAGCCTAGCAGAAGAAGAGATAATAATTAGATCTGAAAATCTGACAAACAATG
TCAAAACAATAATAGTACATCTTAATGAATCTATAGAGATTAAATGTACAAGACC

FIGURE 16

TGGCAATAATACAAGAAAGAGTGTGAGAATAGGACCAGGACAAGCATTCTATGCA
ACAGGAGACATAATAGGAGATATAAGACAAGCACATTGTAACATTAGTAAAAATGA
ATGGAATACAACCTTTACAAAGGGTAAGTCAAAAATTACAAGAACTCTTCCCTAATA
GTACAGGGATAAAAATTTGCACCACACTCAGGAGGGGACCTAGAAATTACTACACAT
AGCTTTAATTGTGGAGGAGAATTTTTCTATTGCAATACAACAGACCTGTTTAATAGT
ACATACAGTAATGGTACATGCACTAATGGTACATGCATGTCTAATAATACAGAGCG
CATCACACTCCAATGCAGAATAAAACAAATTATAAACATGTGGCAGGAGGTAGGAC
GAGCAATGTATGCCCCCTCCATTGCAGGAAACATAACATGTAGATCAAATATTACA
GGACTACTATTAACACGTGATGGAGGAGATAATAACTGAAACAGAGACATTTCAG
ACCTGGAGGAGGAGACATGAGGGACAATTGGAGAAGTGAATTATATAAATACAAG
GTGGTAGAAATTAACCATTAGGAGTAGCACCCACTGCTGCAAAAAGGAGAGTGGT
GGAGAGAGAAAAAAGAGCAGTAGGAATAGGAGCTGTGTTCTTGGGTCTTGGGAG
CAGCAGGAAGCACTATGGGCGCAGCATCAATAACGCTGACGGTACAGGCCAGACAA
TTATTGTCTGGTATAGTGCAACAGCAAAGTAATTTGCTGAGGGCTATAGAGGCGCAA
CAGCATATGTTGCAACTCACGGTCTGGGGCATTAAGCAGCTCCAGGCAAGAGTCCTG
GCTATAGAGAGATACCTACAGGATCAACAGCTCCTAGGACTGTGGGGCTGCTCTGG
AAAACCTCATCTGCACCCTAATGTGCTTTGGAACCTCTAGTTGGAGTAATAAACTCA
AAGTGATATTTGGGATAACATGACCTGGATGCAGTGGGATAGGGAAATTAGTAATT
ACACAAACACAATATACAGGTTGCTTGAAGACTCGCAAAGCCAGCAGGAAAGAAA
TGAAAAAGATTTACTAGCATTGGACAGGTGGAACAATCTGTGGAATTGGTTTAGCAT
AACAAATTGGCTGTGGTATATAAAAATATTCATAATGATAGTAGGAGGCTTGATAG
GTTTAAGAATAATTTTTGCTGTGCTCTCTCTAGTAAATAGAGTTAGGCAGGGATACT
CACCCTTGTCATTGCAGACCCTTATCCCAAACCCGAGGGGACCCGACAGGCTCGGA
GGAATCGAAGAAGAAGGTGGAGAGCAAGACAGCAGCAGATCCATTCGATTAGTGA
GCGGATTCTTGACACTTGCTTGGGACGACCTACGAAGCCTGTGCCTCTTCTGCTACC
ACCGATTGAGAGACTTCATATTAATTGTAGTGAGAGCAGTGGAACCTTCTGGGACAC
AGTAGTCTCAGGGGACTGCAGAGGGGGTGGGGAACCTTAAGTATTTGGGGAGTCT
TGTGCAATATTGGGGTCTAGAGTTAAAAAAGAGTGCTATTAATCTGCTTGATACTAT
AGCAATAGCAGTAGCTGAAGGAACAGATAGGATTCTAGAATTCATACAAAACCTTT
GTAGAGGTATCCGCAACGTACCTAGAAGAATAAGACAGGGCTTCGAAGCAGCTTTG
CAATAAAATGGGGGGCAAGTGGTCAAAAAGCAGTATAATTGGATGGCCTGAAGTAA
GAGAAAGAATCAGACGAACTAGGTCAGCAGCAGAGGGAGTAGGATCAGCGTCTCA
AGACTTAGAGAAACATGGGGCACTTACAACCAGCAACACAGCCCACAACAATGCTG
CTTGCGCCTGGCTGGAAGCGCAAGAGGAGGAAGGAGAAGTAGGCTTTCCAGTCAGA
CCTCAGGTACCTTTAAGACCAATGACTTATAAAGCAGCAATAGATCTCAGCTTCTTT
TTAAAAGAAAAGGGGGGACTGGAAGGGTTAATTTACTCCAAGAAAAGGCAAGAGAT
CCTTGATTTGTGGGTTTATAACACACAAGGCTTCTTCCCTGATTGGCAAACTACAC
ACCGGGACCAGGGGTCAGATTTCCACTGACCTTTGGATGGTACTTCAAGCTAGAGCC
AGTCGATCCAAGGGAAGTAGAAGAGGCCAATGAAGGAGAAAACAACCTGTTTACTAC
ACCCTATGAGCCAGCATGGAATGGAGGATGAAGACAGAGAAGTATTAAGATGGAAG
TTTGACAGTACGCTAGCACGCAGACACATGGCCCGCGAGCTACATCCGGAGTATTAC
AAAGACTGCTGACACAGAAGGGACTTTCCGCTGGGACTTTCCACTGGGGCGTTCCAG
GAGGTGTGGTCTGGGCGGGACAGGGGAGTGGTCAGCCCTGAGATGCTGCATATAAG
CAGCTGCTTTTCGCCTGTACTGGGTCTCTCTAGGTAGACCAGATCTGAGCCCGGGAG

FIGURE 16

CTCTCTGGCTATCTAGGGAACCCACTGCTTAAGCCTCAATAAAGCTTGCCTTGAGTG
CCTTGAGTAGTGTGTGCCCCGTCTGTTGTGTGACTCTGGTAACTAGAGATCCCTCAGA
CCACTTGTGGTAGTGTGGAAAATCTCTAGCA

FIGURE 16

105040-5166850

>C4_Env_TV1_C_ZA_opt_short (SEQ ID NO:46)

CATCACCTGCAGTGCAAGATCAAGCAGATCGTGCGCATGTGGCAGGGCGTGGGCCAGGCCATGTACGCCCCCCCCATCG
CCGGCAACATCACCTGC

FIGURE 17

FIGURE 17

>C4_Env_TV1_C_ZA_opt (SEQ ID NO:47)

CTGCCCATCACCCCTGCAGTGCAAGATCAAGCAGATCGTGCGCATGTGGCAGGGCGTGGGCCAGGCCATGTACGCCCCCCC
CATCGCCGGCAACATCACCTGCCGCAGCAACATCACCGGCATCCTGCTGACCCGCGACGGCGGC

FIGURE 18

FIGURE 18

>C4_Env_TV1_C_ZA_wt (SEQ ID NO:48)

TTACCCATCACACTCCAATGCAAAATAAAACAAATTGTACGCATGTGGCAAGGGGTAGGACAAGCAATGTATGCCCCCTCC
CATTGCAGGAAACATAACATGTAGATCAAACATCACAGGAATACTATTGACACGTGATGGGGGA

FIGURE 19

>Envgp160_TV1_C_ZAopt (SEQ ID NO:49)

ATGCGCGTGATGGGCACCCAGAAGAACTGCCAGCAGTGGTGGATCTGGGGCATCCTGGGCTTCTGGATGCTGATGATCTG
CAACACCGAGGACCTGTGGGTGACCGTGACTACGGCGTGCCCGTGTGGCGCGAGGCCAAGACCACCCTGTTCTGCGCCA
GCGACGCCAAGGCCTACGAGACCGAGGTGCACAACGTGTGGGCCACCCACGCTGCGTGCCACCGACCCCAACCCCGAG
GAGATCGTGCTGGGCAACGTGACCGAGAAGCTTCAACATGTGGAAGAACAACATGGCCGACCAGATGCACGAGGACATCAT
CAGCCTGTGGGACCAGAGCCTGAAGCCCTGCGTGAAGCTGACCCCTGTGCGTGACCTGAACTGCACCGACACCAACG
TGACCGGCAACCGCACCGTGACCGGCAACACCAACGACACCAACATCGCCAACGCCACCTACAAGTACGAGGAGATGAAG
AACTGCAGCTTCAACGCCACCACCGAGCTGCGCGACAAGAAGCACAAGGAGTACGCCCTGTTCTACAAGCTGGACATCGT
GCCCCGTAACGAGAACAGCAACAACCTTACCTACCGCCTGATCAACTGCAACACCAGCACCATCACCCAGGCCTGCCCCA
AGGTGAGCTTCGACCCCATCCCCATCCACTACTGCGCCCCCGCGACTACGCCATCCTGAAGTGCAACAACAAGACCTTC
AACGGCACCGGCCCCCTGCTACAACGTGAGCACCCTGCGTGCAGTGCACCCACGGCATCAAGCCCGTGGTGAGCAACCCAGCTGCT
GCTGAACGGCAGCCTGGCCGAGGAGGGCATCATCATCCGCGAGCGAGAACCTGACCGAGAAACACCAAGACCATCATCGTGC
ACCTGAACGAGAGCGTGAGATCAACTGCACCCGCCCCAACAAACACCCGCAAGAGCGTGCGCATCGGCCCCGGCCAG
GCCTTCTACGCCACCAACGACGTGATCGGCAACATCCGCCAGGCCCACTGCAACATCAGCACCGACCGCTGGAACAAGAC
CCTGCGAGCAGGTGATGAAGAAGCTGGGCGAGCACTTCCCCAACAAAGACCATCAAGTTCGAGCCCCACGCCGGCGCGGACC
TGGAGATCACCATGCACAGCTTCAACTGCCGCGGCGAGTTCTTCTACTGCAACACCAGCAACCTGTTCAACAGCACCTAC
TACCCCAAGAACGGCACCTACAAGTACAACGGCAACAGCAGCCTGCCCATCACCTGCGAGTGAAGATCAAGCAGATCGT
GCGCATGTGGCAGGGCGTGGGCCAGGCCATGTACGCCCCCCCCATCGCCGGCAACATCACCTGCCGCGAGCAACATCACCG
GCATCCTGCTGACCCGCGACGGCGGCTTCAACAACACCAACAACGACACCGAGGAGACCTTCCGCCCCGGCGGCGGCGAC
ATGCGCGACAACCTGGCGCAGCGAGCTGTACAAGTACAAGTGTTGGTGGAGATCAAGCCCTGGGCATCGCCCCACCAAGGC
CAAGCGCCGCGTGGTGACGCGAAGAAGCGCGCCGTGGGCATCGGCGCCGTGTTCTGGGCTTCTGGGCGCCGCGGCA
GCACCATGGGCGCCGCCAGCATCACCTGACCGTGACCGTGACGGCCCGCCAGCTGCTGAGCGGCATCGTGACGAGCAGAGCAAC
CTGCTGAAGGCCATCGAGGCCCAGCAGCACATGCTGACGCTGACCGTGTGGGGCATCAAGCAGCTGCAGGCCCCGCTGCT
GGCCATCGAGCGCTACCTGAAGGACCAGCAGCTGCTGGGCATCTGGGGCTGCAGCGGCCGCTGATCTGCACCACCGCCG
TGCCCTGGAACAGCAGCTGGAGCAACAAGAGCGAGGCCGACATCTGGGACAACATGACCTGGATGCAGTGGGACCGCGAG
ATCAACAACCTACACCGAGACCATCTTCCGCTGCTGGAGGACAGCCAGAACCAGCAGGAGAAGAAGAGAGGACCTGCT
GGAGCTGGACAAGTGGAAACAACCTGTGGAACCTGGTTGACATCAGCAACTGGCTGTGGTACATCAAGATCTTCATCATGA
TCGTGGGCGGCCGTGATCGGCCTGCGCATCATCTTCGCGCTGCTGAGCATCGTGAACCGCGTGCGCCAGGGCTACAGCCCC
CTGAGCTTCCAGACCCTGACCCCCAGCCCCCGCGCCTGGACCGCCTGGGCGGCATCGAGGAGGAGGGCGGCGAGCAGGA
CCGCGACCGCAGCATCCGCCTGGTGAGCGGCTTCTGAGCCTGGCCTGGGACGACCTGCGCAGCCTGTGCCTGTTTACGCT
ACCACCGCCTGCGCGACTTCATCCTGATCGCCGTGCGCGCCGTGGAGCTGCTGGGCCACAGCAGCCTGCGCGGCCTGCAG
CGCGGCTGGGAGATCCTGAAGTACCTGGGCAGCCTGGTGCAGTACTGGGGCTGGAGCTGAAGAAGAGCGCCATCAGCCC
CCTGGACACCATCGCCATCGCCGTGGCCGAGGGCACCGACCGCATCATCGAGCTGGTGCAGCGCATCTGCCGCGCCATCC
TGAACATCCCCCGCCGATCCGCCAGGGCTTCGAGGCCGCCCTGCTGTAA

FIGURE 20

>Envgpl60_TV1_C_ZAwT (SEQ ID NO:50)

ATGAGAGTGATGGGGACACAGAAGAATTGTCAACAATGGTGGATATGGGGCATCTTAGGCTTCTGGATGCTAATGATTTG
TAACACGGAGGACTTGTGGGTCACAGTCTACTATGGGGTACCTGTGTGGAGAGAAGCAAAACTACTCTATTCTGTGCAT
CAGATGCTAAAGCATATGAGACAGAAGTGCATAATGTCTGGGCTACACATGCTTGTGTACCCACAGACCCCAACCCACAA
GAAATAGTTTTGGGAAATGTAACAGAAAATTTTAATATGTGGAAAAATAACATGGCAGATCAGATGCATGAGGATATAAT
CAGTTTATGGGATCAAAGCCTAAAGCCATGTGTAAAGTTGACCCCACTCTGTGTCACTTTAAACTGTACAGATACAAATG
TTACAGGTAATAGAACTGTTACAGGTAATACAAATGATACCAATATTGCAAATGCTACATATAAGTATGAAGAAATGAAA
AATTGCTCTTTCAATGCAACCACAGAATTAAGAGATAAGAAACATAAAGAGTATGCACTCTTTTATAAACTTGATATAGT
ACCACTTAATGAAAATAGTAACAACCTTTACATATAGATTAATAAATTGCAATACCTCAACCATAACACAAGCCTGTCCAA
AGGTCTCTTTTGACCCGATTCTTATACATTACTGTGCTCCAGCTGATTATGCGATTCTAAAGTGAATAATAAGACATTC
AATGGGACAGGACCATGTTATAATGTCAGCACAGTACAATGTACACATGGAATTAAGCCAGTGGTATCAACTCAACTACT
GTTAAATGGTAGTCTAGCAGAAGAAGGGATAATAATTAGATCTGAAAATTTGACAGAGAATACCAAAACAATAATAGTAC
ATCTTAATGAATCTGTAGAGATTAATTGTACAAGGCCCAACAATAATACAAGGAAAAGTGTAAAGGATAGGACCAGGACAA
GCATTCTATGCAACAAATGACGTAATAGGAAACATAAGACAAGCACATTGTAACATTAGTACAGATAGATGGAATAAAAC
TTTACAACAGGTAATGAAAAAATTAGGAGAGCATTTCCCTAATAAAACAATAAAATTTGAACCACATGCAGGAGGGGATC
TAGAAATTACAATGCATAGCTTTAATTGTAGAGGAGAAATTTTCTATTGCAATACATCAAACCTGTTTAATAGTACATAC
TACCTTAAGAATGGTACATACAAATACAATGGTAATTCAAGCTTACCCATCACACTCCAATGCAAAATAAAACAAATTGT
ACGCATGTGGCAAGGGGTAGGACAAGCAATGTATGCCCTCCCATTCAGGAAACATAACATGTAGATCAAACATCACAG
GAATACTATTGACACGTGATGGGGGATTTAACAACACAAACAACGACACAGAGGAGACATTGAGACCTGGAGGAGGAGAT
ATGAGGGATAACTGGAGAAGTGAATTATATAAATATAAAGTGGTAGAAATTAAGCCATTGGGAATAGCACCCACTAAGGC
AAAAAGAAGAGTGGTGCAGAGAAAAAAGAGCAGTGGGAATAGGAGCTGTGTTCTTGGGTTCTTGGGAGCAGCAGGAA
GCACTATGGGCGCAGCGTCAATAACGCTGACGGTACAGGCCAGACAACCTGTTGTCTGGTATAGTGCAACAGCAAAGCAAT
TTGCTGAAGGCTATAGAGGCGCAACAGCATATGTTGCAACTCACAGTCTGGGGCATTAAGCAGCTCCAGGCGAGAGTCTT
GGCTATAGAAAAGATACCTAAAGGATCAACAGCTCCTAGGGATTTGGGGCTGCTCTGGAAGACTCATCTGCACCACTGCTG
TGCCTTGGAATCCAGTTGGAGTAATAAATCTGAAGCAGATATTTGGGATAACATGACTTGGATGCAGTGGGATAGAGAA
ATTAATAATTACACAGAAACAATATTGAGGTTGCTTGAAGACTCGCAAAACCAGCAGGAAAAGAATGAAAAAGATTTATT
AGAATTGGACAAGTGAATAATCTGTGGAATTGGTTTGACATATCAAACCTGGCTGTGGTATATAAAAAATATTCATAATGA
TAGTAGGAGGCTTGATAGGTTTAAGAATAATTTTTGCTGTGCTCTCTATAGTGAATAGAGTTAGGCAGGGATACTCACCT
TTGTCAATTCAGACCCCTTACCCCAAGCCCCGAGGGGACTCGACAGGCTCGGAGGAATCGAAGAAGAAGGTGGAGAGCAAGA
CAGAGACAGATCCATACGATTGGTGAGCGGATTCCTTGTGCTTGCCTGGGACGATCTGCGGAGCCTGTGCCTCTTCAGCT
ACCACCGCTTGAGAGACTTCATATTAATTGCAGTGAGGGCAGTGGAACCTTCTGGGACACAGCAGTCTCAGGGGACTACAG
AGGGGGTGGGAGATCCTTAAGTATCTGGGAAGTCTTGTGCAGTATTGGGGTCTAGAGCTAAAAAAGAGTGCATTATAGTCC
GCTTGATACCATAGCAATAGCAGTAGCTGAAGGAACAGATAGGATTATAGAATTGGTACAAAGAATTTGTAGAGCTATCC
TCAACATACCTAGGAGAATAAGACAGGGCTTTGAAGCAGCTTTGCTATAA

FIGURE 21

>Gag_TV1_C_ZAopt (SEQ ID NO:51)

ATGGGCGCCCGCGCCAGCATCCTGAGCGGCGGCAAGCTGGACAAGTGGGAGCGCATCCGCCTGCGCCCCGGCGGCAAGAA
GCACTACATGCTGAAGCACCTGGTGTGGGCCAGCCGCGAGCTGGAGCGCTTCGCCCTGAACCCCGGCCCTGCTGGAGACCA
GCGAGGGCTGCAAGCAGATCATCAAGCAGCTGCAGCCCGCCCTGCAGACCGGCACCGAGGAGCTGCGCAGCCTGTTCAAC
ACCGTGGCCACCCTGTACTGCGTGCACAAGGGCATCGAGGTGCGCGACACCAAGGAGGCCCTGGACAAGATCGAGGAGGA
GCAGAACAAGTGCCAGCAGAAGGCCAGCAGGCCAAGGCCGCGACGAGAAGGTGAGCCAGAACTACCCCATCGTGCAGA
ACGCCCAGGGCCAGATGGTGCACCAGGCCATCAGCCCCCGCACCTGAACGCCTGGATCAAGGTGATCGAGGAGAAGGCC
TTCAACCCCGAGGAGATCCCCATGTTCAACGCCCTGAGCGAGGGCGCCACCCCCAGGACCTGAACACCATGCTGAACAC
CGTGGGCGGCCACCAGGCCGCCATGCAGATGCTGAAGGACACCATCAACGAGGAGGCCGCGGAGTGGGACCGCACCCACC
CCGTGCACGCGCGCCCGTGGCCCCCGGCCAGATGCGCGAGCCCCGCGGCAGCGACATCGCCGGCACCCAGCACCCCTG
CAGGAGCAGATCGCCTGGATGACCAGCAACCCCCCATCCCCGTGGAGGACATCTACAAGCGCTGGATCACTCCTGGGCCT
GAACAAGATCGTGCATGTACAGCCCCGTGAGCATCCTGGACATCAAGCAGGGCCCCAAGGAGCCCTTCCGCGACTACG
TGGACCGCTTCTTCAAGACCCTGCGCGCCGAGCAGGCCACCCAGGACGTGAAGAACTGGATGACCGACACCCTGCTGGTG
CAGAACGCCAACCCCGACTGCAAGACCATCCTGCGCGCCCTGGGCCCCGGCGCCAGCCTGGAGGAGATGATGACCGCCTG
CCAGGGCGTGGGCGGCCCCAGCCACAAGGCCCGCGTGTGGCCGAGGCCATGAGCCAGGCCAACAGCAACATCCTGGTGC
AGCGCAGCAACTTCAAGGGCAGCAACCGCATCATCAAGTGCTTCAACTGCGGCAAGGTGGGCCACATCGCCCGCAACTGC
CGCGCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCCAGGAGGGCCACCAGATGAAGGACTGCACCGAGCGCCAGGCCAA
CTTCCTGGGCAAGATCTGGCCAGCCACAAGGGCCGCCCCGGCAACTTCTGCGAGAACCGCCCCGAGCCCCACCGCCCCC
CCGCCGAGCCCACCGCCCCCCCCCGCCGAGAGCTTCCGCTTCGAGGAGACCACCCCGTGCCCCGCAAGGAGAAGGAGCGC
GAGCCCCTGACCAGCCTGAAGAGCCTGTTCCGGCAGCGACCCCTGAGCCAGTAA

FIGURE 22

>Gag_TV1_C_ZAwT (SEQ ID NO:52)

ATGGGTGCGAGAGCGTCAATATTAAGCGGCGGAAAATTAGATAAATGGGAAAGAATTAGGTTAAGGCCAGGGGGAAAGAA
ACATTATATGTTAAAACATCTAGTATGGGCAAGCAGGGAGCTGGAAAGATTTGCACTTAACCCTGGCCTGTTAGAAACAT
CAGAAGGCTGTAAACAAATAATAAAACAGCTACAACCAGCTCTTCAGACAGGAACAGAGGAACTTAGATCATTATTCAAC
ACAGTAGCAACTCTCTATTGTGTACATAAAGGGATAGAGGTACGAGACACCAAGGAAGCCTTAGACAAGATAGAGGAAGA
ACAAAACAAATGTCAGCAAAAAGCACAAACAGGCAAAAGCAGCTGACGAAAAGGTCAGTCAAAATTATCCTATAGTACAGA
ATGCCCAGGGCAAATGGGTACACCAAGCTATATCACCTAGAACATTGAATGCATGGATAAAAGTAATAGAGGAAAAGGCT
TTCAATCCAGAGGAAATACCCATGTTTACAGCATTATCAGAAGGAGCCACCCACAAGATTTAAACACAATGTTAAATAC
AGTGGGGGGACATCAAGCAGCCATGCAAATGTTAAAAGATACCATCAATGAGGAGGCTGCAGAATGGGATAGGACACATC
CAGTACATGCAGGGCCTGTTGCACCAGGCCAGATGAGAGAACCAAGGGGAAGTGACATAGCAGGAACTACTAGTACCCTT
CAGGAACAAATAGCATGGATGACAAGTAATCCACCTATTCCAGTAGAAGACATCTATAAAAGATGGATAATTCTGGGGTT
AAATAAAATAGTAAGAATGTATAGCCCTGTTAGCATTTTGGACATAAAACAAGGGCCAAAAGAACCCTTTAGAGACTATG
TAGACCGGTTCTTTAAAACCTTAAGAGCTGAACAAGCTACACAAGATGTAAAGAATTGGATGACAGACACCTTGTTGGTC
CAAAATGCGAACCCAGATTGTAAGACCATTTTAAGAGCATTAGGACCAGGGGCCTCATTAGAAGAAATGATGACAGCATG
TCAGGGAGTGGGAGGACCTAGCCATAAAGCAAGAGTGTTGGCTGAGGCAATGAGCCAAGCAAACAGTAACATACTAGTGC
AGAGAAGCAATTTTAAAGGCTCTAACAGAATTATTAAATGTTTCACTGTGGCAAAGTAGGGCACATAGCCAGAAATTGC
AGGGCCCCCTAGGAAAAAGGGCTGTTGGAAATGTGGACAGGAAGGACACCAAATGAAAGACTGTACTGAGAGGCAGGCTAA
TTTTTTAGGGAAAATTTGGCCTTCCCACAAGGGGAGGCCAGGGAATTTCTCCAGAACAGACCAGAGCCAACAGCCCCAC
CAGCAGAACCAACAGCCCCACCAAGCAGAGAGCTTCAGGTTTCGAGGAGACAACCCCCGTGCCGAGGAAGGAGAAAGAGAGG
GAACCTTTAACTTCCCTCAAATCACTCTTTTGGCAGCGACCCCTTGCTCAATAA

FIGURE 23

10330"345660

>Gag_TV1_ZA_MHROpt (SEQ ID NO:53)

GACATCAAGCAGGGCCCCAAGGAGCCCTTCGCGACTACGTGGACCGCTTCTTCAAGACC

FIGURE 24

FIGURE 24

>Gag_TV1_ZA_MHRwt (SEQ ID NO:54)

GACATAAAACAAGGGCCAAAAGAACCCTTTAGAGACTATGTAGACCGGTTCTTTAAAACC

FIGURE 25

1050/0" 1156660

>Nef_TV1_C_ZAopt (SEQ ID NO:55)

ATGGGCGGCAAGTGGAGCAAGCGCAGCATCGTGGGCTGGCCCGCCGTGCGCGAGCGCATGCGCCGCACCGAGCCCGCCGC
CGAGGGCGTGGGCGCCGCCAGCCAGGACCTGGACCGCCACGGCGCCCTGACCAGCAGCAACACCCCGCCACCAACGAGG
CCTGCGCCTGGCTGCAGGCCCAGGAGGAGGACGGCGACGTGGGCTTCCCCGTGCGCCCCCAGGTGCCCCCTGCGCCCCATG
ACCTACAAGAGCGCCGTGGACCTGAGCTTCTTCCTGAAGGAGAAGGGCGGCCTGGAGGGCCTGATCTACAGCCGCAAGCG
CCAGGAGATCCTGGACCTGTGGGTGTACAACACCCAGGGCTTCTTCCCCGACTGGCAGAACTACACCAGCGGCCCCGGCG
TGCGCTTCCCCCTGACCTTCGGCTGGTGCTTCAAGCTGGTGCCCGTGGACCCCGCGAGGTGAAGGAGGCCAACGAGGGC
GAGGACAATGCCTGCTGCACCCCATGAGCCAGCACGGCGCCGAGGACGAGGACCGCGAGGTGCTGAAGTGAAGTTCTGA
CAGCCTGCTGGCCACCGCCACATGGCCCGCGAGCTGCACCCCGAGTACTACAAGGACTGCTGA

FIGURE 26

FIGURE 26

>NefD125G_TV1_C_ZAopt (SEQ ID NO:57)

ATGGGCGGCAAGTGGAGCAAGCGCAGCATCGTGGGCTGGCCCGCCGTGCGCGAGCGCATGCGCCGCACCGAGCCCGCCGC
CGAGGGCGTGGGCGCCGCCAGCCAGGACCTGGACCGCCACGGCGCCCTGACCAGCAGCAACACCCCGCCACCAACGAGG
CCTGCGCCTGGCTGCAGGCCCAGGAGGAGGACGGCGACGTGGGCTTCCCCGTGCGCCCCCAGGTGCCCCCTGCGCCCCATG
ACCTACAAGAGCGCCGTGGACCTGAGCTTCTTCCTGAAGGAGAAGGGCGGCCTGGAGGGCCTGATCTACAGCCGCAAGCG
CCAGGAGATCCTGGACCTGTGGGTGTACAACACCCAGGGCTTCTTCCCCGGCTGGCAGAACTACACCAGCGGCCCCGGCG
TGCGCTTCCCCCTGACCTTCGGCTGGTGCTTCAAGCTGGTGCCCGTGGACCCCGCGAGGTGAAGGAGGCCAACGAGGGC
GAGGACAACCTGCCTGCTGCACCCCATGAGCCAGCACGGCGCCGAGGACGAGGACCGCGAGGTGCTGAAGTGAAGTTCGA
CAGCCTGCTGGCCCAACGCCACATGGCCCGCGAGCTGCACCCCGAGTACTACAAGGACTGCTGA

FIGURE 28

FIGURE 28

>p15RNaseH_TV1_C_ZAopt (SEQ ID NO:58)

ACCTTCTACGTGGACGGCGCCACCAACCGCGAGGCCAAGATCGGCAAGGCCGGCTACGTGACCGACCGCGGCCGAGAA
GATCGTGACCCTGACCAACACCACCAACCAGAAGACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGGCAGCG
AGGTGAACATCGTGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCAGCCGACAAGAGCGACAGCGAGATCTTC
AACCAGATCATCGAGCAGCTGATCAACAAGGAGCGCATCTACCTGAGCTGGGTGCCCGCCACAAGGGCATCGGCCGGCAA
CGAGCAGGTGGACAAGCTGGTGAGCAAGGGCATC

FIGURE 29

FIGURE 29

>p15RNaseH_TV1_C_Zawt (SEQ ID NO:59)

ACTTTCTATGTAGATGGAGCAACTAATAGGGAAGCTAAAATAGGAAAAGCAGGGTATGTTACTGACAGAGGAAGGCAGAA
AATTGTTACTCTAACTAACACAACAAATCAGAAGACTGAGTTACAAGCAATTCAGCTAGCTCTGCAGGATTCAGGATCAG
AAGTAAACATAGTAACAGACTCACAGTATGCATTAGGAATCATTCAAGCACACCAGATAAGAGTGACTCAGAGATATTT
AACCAAATAATAGAACAGTTAATAAAACAAGGAAAGAATCTACCTGTCATGGGTACCAGCACATAAAGGAATTGGGGGAAA
TGAACAAGTAGATAAATTAGTAAGTAAGGGAATT

FIGURE 30

FIGURE 30

>p31Int_TV1_C_Zaopt (SEQ ID NO:60)

CGCAAGGTGCTGTTCTGGACGGCATCGACAAGGCCAGGAGGAGCAGAGCGCTACACAGCAACTGGCGCGCCATGGC
CAACGAGTTCAACCTGCCCCCATCGTGGCCAAGGAGATCGTGGCCAGCTGCGACAAGTGCCAGCTGAAGGGCGAGGCCA
TCCACGGCCAGGTGGACTGCAGCCCCGGCATCTGGCAGCTGGACTGCACCCACCTGGAGGGCAAGATCATCCTGGTGGCC
GTGCACGTGGCCAGCGGTACATGGAGGCCGAGGTGATCCCCGCCGAGACCGGCCAGGAGACCGCCTACTTCATCCTGAA
GCTGGCCGGCCGCTGGCCCGTGAAGGTGATCCACACCGACAACGGCAGCAACTTCACCAGCACCGCCGTGAAGGCCGCCT
GCTGGTGGGCCGGCATCCAGCAGGAGTTCGGCATCCCCACAACCCCCAGAGCCAGGGCGTGGTGGAGAGCATGAACAAG
GAGCTGAAGAAGATCATCGGCCAGGTGCGCGACCAGGCCGAGCACCTGAAGACCGCCGTGCAGATGGCCGTGTTTCATCCA
CAACTTCAAGCGCAAGGGCGGCATCGGCGGCTACAGCGCCGGCGAGCGCATCATCGACATCATCGCCACCGACATCCAGA
CCAAGGAGCTGCAGAAGCAGATCATCCGCATCCAGAACTTCCGCGTGACTACCGCGACAGCCGCGACCCCATCTGGAAG
GGCCCCGCCGAGCTGCTGTGGAAGGGCGAGGGCGTGGTGGTGATCGAGGACAAGGGCGACATCAAGGTGGTGGCCCCGCC
CAAGGCCAAGATCATCCGCGACTACGGCAAGCAGATGGCCGGCGCCGACTGCGTGGCCGGCGGCCAGGACGAGGAC

FIGURE 31

FIGURE 31

>p31Int_TV1_C_ZAwt (SEQ ID NO:61)

AGGAAAGTGTTGTTTCTAGATGGAATAGATAAAGCTCAAGAAGAGCATGAAAGGTACCACAGCAATTGGAGAGCAATGGC
TAATGAGTTTAATCTGCCACCCATAGTAGCAAAAGAAATAGTAGCTAGCTGTGATAAATGTCAGCTAAAAGGGGAAGCCA
TACATGGACAAGTCGACTGTAGTCCAGGGATATGGCAATTAGATTGTACCCATTTAGAGGGAAAAATCATCCTGGTAGCA
GTCCATGTAGCTAGTGGCTACATGGAAGCAGAGGTTATCCAGCAGAAACAGGACAAGAAACAGCATATTTTATATTAAA
ATTAGCAGGAAGATGGCCAGTCAAAGTAATACATACAGACAATGGCAGTAATTTTACCAGTACTGCAGTTAAGGCAGCCT
GTTGGTGGGCAGGTATCCAACAGGAATTTGGAATTCCTTACAATCCCCAAAGTCAGGGAGTGGTAGAATCCATGAATAAA
GAATTAAAGAAAAATAATAGGACAAGTAAGAGATCAAGCTGAGCACCTTAAGACAGCAGTACAAATGGCAGTATTCATTCA
CAATTTTAAAGAAAAAGGGGAATTGGGGGTACAGTGCAGGGGAAAGAATAATAGACATAATAGCAACAGACATACAAA
CTAAAGAATTACAAAAACAAATTATAAGAATTCAAAATTTTCGGGTTTATTACAGAGACAGCAGAGACCCTATTTGGAAA
GGACCAGCCGAACACTACTCTGGAAAGGTGAAGGGGTAGTAGTAATAGAAGATAAAGGTGACATAAAGGTAGTACCAAGGAG
GAAAGCAAAAATCATTAGAGATTATGGAAAACAGATGGCAGGTGCTGATTGTGTGGCAGGTGGACAGGATGAAGAT

FIGURE 32

FIGURE 32

>Pol_TV1_C_ZAopt (SEQ ID NO:62)

TTCTTCCGCGAGAACCTGGCCTTCCCCAGGGCGAGGCCCGCGAGTTCCCCCGAGCAGACCCGCGCCAACAGCCCCAC
CAGCCGCACCAACAGCCCCACCAGCCGCGAGCTGCAGGTGCGCGGCGACAACCCCGCGCCGAGGAGGGCGAGCGCGAGG
GCACCTTCAACTTCCCCCAGATCACCTGTGGCAGCGCCCCCTGGTGAGCATCAAGGTGGAGGGCCAGATCAAGGAGGCC
CTGCTGGACACCGGCGCCGACGACACCGTGCTGGAGGAGATCGACCTGCCCGGCAAGTGGAAGCCCAAGATGATCGGCGG
CATCGGCGGCTTCATCAAGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCGTG
TGGTGGGCCCCACCCCGTGAACATCATCGGCCGCAACCTGCTGACCCAGCTGGGCTGCACCCCTGAACCTTCCCCATCAGC
CCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCCGGCATGGACGGCCCCAAGGTGAAGCAGTGGCCCCCTGACCGAGGAGAA
GATCAAGGCCCTGACCGCCATCTGCGAGGAGATGGAGAAGGAGGGCAAGATCACCAAGATCGGCCCGGACAAACCCCTACA
ACACCCCGTGTTTCGCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGGACTTCCGCGAGCTGAACAAGCGC
ACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCACCCCGCGGCTGAAGAAGAAGAAGAGCGTGACCGTGCTGGA
CGTGGGCGACGCTACTTCAGCGTGCCCTGGACGAGAGCTTCCGCAAGTACACCGCCTTACCATCCCCAGCATCAACA
ACGAGACCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCAGCCCCGCCATCTTCCAGAGCAGC
ATGACCAAGATCCTGGAGCCCTTCCGCGCCAAGAACCCGACATCGTGATCTACCAGTACATGGACGACCTGTACGTGGG
CAGCGACCTGGAGATCGGCCAGCACCGCGCAAGATCGAGGAGCTGCGCGAGCACCTGCTGAAGTGGGGCTTACCACCC
CCGACAAGAAGCACCAGAAGGAGCCCCCTTCTGTGGATGGGCTACGAGCTGCACCCCGACAAGTGGACCGTGCAGCCC
ATCCTGCTGCCCAGAGAAGGACAGCTGACCGTGAACGACATCCAGAAGCTGGTGGGCAAGCTGAACCTGGGCCAGCCAGAT
CTACCCCGGCATCAAGGTGCGCCAGCTGTGCAAGCTGCTGCGCGCGCCAAGGCCCTGACCGACATCGTGCCCCTGACCG
AGGAGGCCGAGCTGGAGCTGGCCGAGAACC GCGAGATCCTGCGCGAGCCCGTGACGGCGTGTACTACGACCCAGCAAG
GACCTGATCGCCGAGATCCAGAAGCAGGGCCACGAGCAGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAA
GACCGGCAAGTACGCCAAGATGCGCACCAACCCACACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCA
TGGAGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCTGCCCATCCAGAAGGAGACCTGGGAGACCTGGTGGACC
GACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTTCTGTAACACCCCCCTGGTGAAGCTGTGGTACCAGCTGGA
GAAGGACCCCATCGCCGGCGTGGAGACCTTCTACGTGGACGGCGCCACCAACCGCGAGGCCAAGATCGGCAAGGCCGGCT
ACGTGACCGACCGCGGCCGCGCAGAAGATCGTGACCCTGACCAACACCACCAACCAGAAGACCGAGCTGCAGGCCATCCAG
CTGGCCCTGCAGGACAGCGGCAGCGAGGTGAACATCGTGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCAGCC
CGACAAGAGCGACAGCGAGATCTTCAACCAGATCATCGAGCAGCTGATCAACAAGGAGCGCATCTACCTGAGCTGGGTGC
CCGCCCACAAGGGCATCGGCGGCAACGAGCAGGTGGACAAGCTGGTGAGCAAGGGCATCCGCAAGGTGCTGTTCCTGGAC
GGCATCGACAAGGCCAGGAGGAGCAGGAGCGCTACCACAGCAACTGGCGCGCCATGGCCAACGAGTTCAACCTGCCCC
CATCGTGGCCAAGGAGATCGTGGCCAGCTGCGACAAGTGCCAGCTGAAGGGCGAGGCCATCCACGGCCAGGTGGACTGCA
GCCCCGGCATCTGGCAGCTGGACTGCACCCACCTGGAGGGCAAGATCATCCTGGTGGCCGTGCACGTGGCCAGCGGCTAC
ATGGAGGCCGAGGTGATCCCCGCGAGACCGGCCAGGAGACCGCCTACTTCATCCTGAAGCTGGCCGGCCGCTGGCCCGT
GAAGGTGATCCACACCGACAACGGCAGCAACTTACCAGACCGCCGTGAAGGCCGCTGCTGGTGGCCGGCATCCAGC
AGGAGTTCGGCATCCCCTACAACCCCGAGGCCAGGGCGTGGTGGAGAGCATGAACAAGGAGCTGAAGAAGATCATCGGC
CAGGTGCGCGACACAGGCCGAGCACCTGAAGACCGCCGTGCAGATGGCCGTGTTTCATCCACAACCTTCAAGCGCAAGGGCGG
CATCGGCGGCTACAGCGCCGGGAGCGCATCATCGACATCATCGCCACCGACATCCAGACCAAGGAGCTGCAGAAGCAGA
TCATCCGCATCCAGAACCTTCCGCGTGTACTACCGCGACAGCCGCGACCCCATCTGGAAGGGCCCCCGGAGCTGCTGTGG
AAGGGCGAGGGCGTGGTGGTATCGAGGACAAGGGCGCATCAAGGTGGTGCCCCCGCGCAAGGCCAAGATCATCCGCGA
CTACGGCAAGCAGATGGCCGGCGCGGACTGCGTGCCGGCGGGCCAGGACGAGGAC

FIGURE 33

>Pol_TV1_C_ZAwT (SEQ ID NO:63)

TTTTTTAGGGAAAATTTGGCCTTCCCAAGGGGAGGCCAGGGAATTTCTCCAGAACAGACCAGAGCCAACAGCCCCAC
CAGCAGAACCAACAGCCCCACCAGCAGAGAGCTTCAGGTTTCGAGGAGACAACCCCCGTGCCGAGGAAGGAGAAAAGAGAGG
GAACCTTTAACTTCCCTCAAATCACTCTTTGGCAGCGACCCCTTGTCTCAATAAAAAGTAGAGGGCCAGATAAAGGAGGCT
CTCTTAGACACAGGAGCAGATGATACAGTATTAGAAGAAATAGATTTGCCAGGGAAATGGAAACCAAAATGATAGGGGG
AATTGGAGGTTTTATCAAAGTAAGACAGTATGATCAAATACTTATAGAAAATTTGTGGAAAAAAGGCTATAGGTACAGTAT
TAGTAGGGCCTACACCAGTCAACATAATTGGAAGAAATCTGTTAACTCAGCTTGGATGCACACTAAATTTTCCAATTAGT
CCTATTGAACTGTACCAGTAAAATTAAAACCAGGAATGGATGGCCCAAAGGTCAAACAATGGCCATTGACAGAAGAAAA
AATAAAAGCATTAAACAGCAATTTGTGAGGAAATGGAGAAGGAAGGAAAAATTACAAAAATTGGGCCTGATAATCCATATA
ACACTCCAGTATTTGCCATAAAAAAGAGGACAGTACTAAGTGGAGAAAAATTAGTAGATTTTCAGGGAACTCAATAAAAGA
ACTCAAGACTTTTGGGAAGTTCAATTAGGAATACCACACCCAGCAGGATTAaaaaaagaaaaaatCAGTGACAGTGCTAGA
TGTGGGGGATGCATATTTTTTCAGTTCCTTTAGATGAAAGCTTCAGGAAATATACTGCATTACCATACCTAGTATAAAACA
ATGAAACACCAGGGATTAGATATCAATATAATGTGCTGCCACAGGGATGGAAAGGATCACCAGCAATATTCAGAGTAGC
ATGACAAAAATCTTAGAGCCCTTCAGAGCAAAAAATCCAGACATAGTTATCTATCAATATATGGATGACTTGTATGTAGG
ATCTGACTTAGAAATAGGGCAACATAGAGCAAAAAATAGAAGAGTTAAGGGAACATTTATTGAAATGGGGATTACAAACAC
CAGACAAGAAACATCAAAAAGAACCCCCATTTCTTTGGATGGGGTATGAACTCCATCCTGACAAATGGACAGTACAACCT
ATACTGCTGCCAGAAAAGGATAGTTGGACTGTCAATGATATACAGAAAGTTAGTGGGAAAATTAACCTGGGCAAGTCAGAT
TTACCCAGGGATTAAAGTAAGGCAACTCTGTAAACTCCTCAGGGGGGCCAAAGCACTAACAGACATAGTACCACTAACTG
AAGAAGCAGAATTAGAATTGGCAGAGAACAGGGGAAATTTTAAGAGAACCAGTACATGGAGTATATTATGATCCATCAAAA
GACTTGATAGCTGAAATACAGAAACAGGGGCATGAACAATGGACATATCAAATTTATCAAGAACCATTTAAAAATCTGAA
AACAGGGAAGTATGCAAAAATGAGGACTACCCACACTAATGATGTAAACAGTTAACAGAGGCAGTGCAAAAAATAGCCA
TGGAAAGCATAGTAATATGGGGAAAGACTCCTAAATTTAGACTACCCATCCAAAAAGAAACATGGGAGACATGGTGGACA
GACTATTGGCAAGCCACCTGGATCCCTGAGTGGGAGTTTGTTAATACCCCTCCCTAGTAAAATTATGGTACCAACTAGA
AAAAGATCCCATAGCAGGAGTAGAAAACTTTCTATGTAGATGGAGCAACTAATAGGGAAGCTAAAATAGGAAAAGCAGGGT
ATGTTACTGACAGAGGAAGGCAGAAAATTTGTTACTCTAACTAACACAACAAATCAGAAGACTGAGTTACAAGCAATTCAG
CTAGCTCTGCAGGATTACAGGATCAGAAGTAAACATAGTAACAGACTCACAGTATGCATTAGGAATCATTCAGCACAAACC
AGATAAGAGTGACTCAGAGATATTTAACCATAATAGAACAGTTAATAACAAGGAAAGAATCTACCTGTCATGGGTAC
CAGCACATAAAGGAATTGGGGGAAATGAACAAGTAGATAAATTAGTAAGTAAGGGAATTAGGAAAGTGTGTTTCTAGAT
GGAATAGATAAAGCTCAAGAAGAGCATGAAAGGTACCACAGCAATTGGAGAGCAATGGCTAATGAGTTTAACTGCGCAC
CATAGTAGCAAAAGAAATAGTAGCTAGCTGTGATAAATGTCAGCTAAAAGGGGAAGCCATACATGGACAAGTCGACTGTA
GTCCAGGGATATGGCAATTAGATTGTACCCATTTAGAGGGAAAAATCATCCTGGTAGCAGTCCATGTAGCTAGTGGCTAC
ATGGAAGCAGAGGTTATCCAGCAGAAACAGGACAAGAAACAGCATATTTTATATTTAAATTTAGCAGGAAGATGGCCAGT
CAAAGTAATACATACAGACAATGGCAGTAATTTTACCAGTACTGCAGTTAAGGCAGCCTGTTGGTGGGCAGGTATCCAAC
AGGAATTTGGAATTCCTACAATCCCCAAAGTCAGGGAGTGGTAGAATCCATGAATAAAGAATTAAAGAAAAATAATAGGA
CAAGTAAGAGATCAAGCTGAGCACCTTAAGACAGCAGTACAAATGGCAGTATTCATTCACAATTTTAAAGAAAAGGGGG
AATTGGGGGGTACAGTGCAGGGGAAAGAATAATAGACATAATAGCAACAGACATACAACTAAAGAATTACAAAAACAAA
TTATAAGAATTCAAAATTTTCGGGTTTATTACAGAGACAGCAGAGACCCATTTTGGAAAGGACCAGCCGAACACTCTGG
AAAGGTGAAGGGGTAGTAGTAATAGAAGATAAAGGTGACATAAAGGTAGTACCAAGGAGGAAAGCAAAAATCATTAGAGA
TTATGGAAAACAGATGGCAGGTGCTGATTGTGTGCAGGTGGACAGGATGAAGAT

FIGURE 34

>Prot_TV1_C_ZAopt (SEQ ID NO:64)

CCCCAGATCACCCGTGTGGCAGCGCCCCCTGGTGAGCATCAAGGTGGAGGGCCAGATCAAGGAGGCCCTGCTGGACACCGG
CGCCGACGACACCGTGCTGGAGGAGATCGACCTGCCCCGGCAAGTGAAGCCCAAGATGATCGGCGGCATCGGCGGCTTCA
TCAAGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCGTGCTGGTGGGCCCCACC
CCCGTGAACATCATCGGCCGCAACCTGCTGACCCAGCTGGGCTGCACCCTGAACTTC

FIGURE 35

FIGURE 35

>Prot_TV1_C_ZAwT (SEQ ID NO:65)

CCTCAAATCACTCTTTGGCAGCGACCCCTTGTCTCAATAAAAGTAGAGGGCCAGATAAAGGAGGCTCTCTTAGACACAGG
AGCAGATGATACAGTATTAGAAGAAATAGATTTGCCAGGGAAATGGAAACCAAAAATGATAGGGGGAATTGGAGGTTTTA
TCAAAGTAAGACAGTATGATCAAATACTTATAGAAATTTGTGGAAAAAAGGCTATAGGTACAGTATTAGTAGGGCCTACA
CCAGTCAACATAATTGGAAGAAATCTGTAACTCAGCTTGGATGCACACTAAATTTT

FIGURE 36

1030203256860

>Protina_TV1_C_ZAopt (SEQ ID NO:66)

CCCCAGATCACCTGTGGCAGCGCCCCCTGGTGAGCATCAAGGTGGAGGGCCAGATCAAGGAGGCCCTGCTGGCCACCGG
CGCCGACGACACCGTGCTGGAGGAGATCGACCTGCCCGGCAAGTGAAGCCCAAGATGATCGGCGGCATCGGCGGCTTCA
TCAAGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCGTGCTGGTGGGCCCCACC
CCCGTGAACATCATCGGCCGCAACCTGCTGACCCAGCTGGGCTGCACCTGAACTTC

FIGURE 37

FIGURE 37

>Protina_TV1_C_ZAwT (SEQ ID NO:67)

CCTCAAATCACTCTTTGGCAGCGACCCCTTGTCTCAATAAAAGTAGAGGGCCAGATAAAGGAGGCTCTCTTAGCCACAGG
AGCAGATGATACAGTATTAGAAGAAATAGATTTGCCAGGGAAATGGAAACCAAAATGATAGGGGGAATTGGAGGTTTTA
TCAAAGTAAGACAGTATGATCAAATACTTATAGAAATTTGTGGAAAAAAGGCTATAGGTACAGTATTAGTAGGGCCTACA
CCAGTCAACATAATTGGAAGAAATCTGTAACTCAGCTTGGATGCACACTAAATTTT

FIGURE 38

FIGURE 38

>ProtinaRTmut_TV1_C_ZAopt (SEQ ID NO:68)

CCCCAGATCACCTGTGGCAGCGCCCCCTGGTGAGCATCAAGGTGGAGGGCCAGATCAAGGAGGCCCTGCTGGCCACCGG
CGCCGACGACACCGTGCTGGAGGAGATCGACCTGCCCCGCAAGTGGAAGCCCAAGATGATCGGCGGCATCGGCGGCTTCA
TCAAGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCGTGCTGGTGGGCCCCACC
CCCGTGAACATCATCGGCCGCAACCTGCTGACCCAGCTGGGCTGCACCCCTGAACTTCCCCATCAGCCCCATCGAGACCGT
GCCCCGTGAAGCTGAAGCCCGGCATGGACGGCCCCAAGGTGAAGCAGTGGCCCCCTGACCGAGGAGAAGATCAAGGCCCTGA
CCGCCATCTGCGAGGAGATGGAGAAGGAGGGCAAGATCACCAAGATCGGCCCCGACAACCCCTACAACACCCCGTGTTTC
GCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGGACTTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTG
GGAGGTGCAGCTGGGCATCCCCACCCCGCCGGCCTGAAGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGGCGACGCCT
ACTTCAGCGTGCCCCCTGGACGAGAGCTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCAACAACGAGACCCCCGGC
ATCCGCTACCAAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCAGCCCCGCCATCTTCCAGAGCAGCATGAACAAGATCCT
GGAGCCCTTCCGCGCCAAGAACCCCGACATCGTGATCTACCAGGCCCCCTGTACGTGGGCAGCGACCTGGAGATCGGCC
AGCACCGCGCCAAGATCGAGGAGCTGCGCGAGCACCTGCTGAAGTGGGGCTTACCACCCCGACAAGAAGCACCAGAAG
GAGCCCCCTTCTGCCCATCGAGCTGCACCCCGACAAGTGGACCGTGACGCCCCATCTGCTGCCCCGAGAAGGACAGCTG
GACCGTGAAACGACATCCAGAAGCTGGTGGGCAAGCTGAACTGGGCCAGCCAGATCTACCCCGGCATCAAGGTGCGCCAGC
TGTGCAAGCTGCTGCGCGGCGCCAAGGCCCTGACCGACATCGTGCCCCTGACCGAGGAGGCCGAGCTGGAGCTGGCCGAG
AACCGCGAGATCCTGCGCGAGCCCGTGACGGCGTGTACTACGACCCAGCAAGGACCTGATCGCCGAGATCCAGAAGCA
GGGCCACGAGCAGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCCTGAAGACCGGCAAGTACGCCAAGATGCGCA
CCACCCACACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCATGGAGAGCATCGTGATCTGGGGCAAG
ACCCCAAGTTCCGCTGCCCATCCAGAAGGAGACCTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCC
CGAGTGGGAGTTCTGTAACACCCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGACCCCATCGCCGGCGTGGAGA
CCTTCTACGTGGACGGCGCCACCAACCGCGAGGCCAAGATCGGCAAGGCCGGCTACGTGACCGACCGCGGCCGCGCAGAAG
ATCGTGACCCCTGACCAACACCACCAACCAGAAGACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGGCAGCGA
GGTGAACATCGTGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCAGCCCGACAAGAGCGACAGCGAGATCTTCA
ACCAGATCATCGAGCAGCTGATCAACAAGGAGCGCATCTACCTGAGCTGGGTGCCCGCCACAAGGGCATCGGCGGCAAC
GAGCAGGTGGACAAGCTGGTGGCAAGGGCATCCGCAAGGTGCTG

FIGURE 39

>ProtinaRTmut_TV1_C_ZAwt (SEQ ID NO:69)

CCTCAAATCACTCTTTGGCAGCGACCCCTTGTCTCAATAAAAGTAGAGGGCCAGATAAAGGAGGCTCTCTTAGCCACAGG
AGCAGATGATACAGTATTAGAAGAAATAGATTTGCCAGGGAAATGGAAACCAAAATGATAGGGGGAATTGGAGGTTTTA
TCAAAGTAAGACAGTATGATCAAATACTTATAGAAATTTGTGGAAAAAGGCTATAGGTACAGTATTAGTAGGGCCTACA
CCAGTCAACATAATTGGAAGAAATCTGTTAACTCAGCTTGATGCACACTAAATTTTCCAATTAGTCCTATTGAACTGT
ACCAGTAAATTTAAACCAGGAATGGATGGCCCAAAGGTCAAACAATGGCCATTGACAGAAGAAAAATAAAGCATTAA
CAGCAATTTGTGAGGAAATGGAGAAGGAAGGAAAAATTACAAAAATTGGGCCTGATAATCCATATAACACTCCAGTATTT
GCCATAAAAAAGAAGGACAGTACTAAGTGGAGAAAAATTAGTAGATTTTCAGGGAACTCAATAAAAGAAGTCAAGACTTTTG
GGAAGTTCAATTAGGAATACCACACCCAGCAGGATTAAAAAAGAAAAATCAGTGACAGTGCTAGATGTGGGGGATGCAT
ATTTTTTCAGTTCCTTTAGATGAAAGCTTCAGGAAATATACTGCATTACCATACCTAGTATAAACAATGAAACACCAGGG
ATTAGATATCAATATAATGTGCTGCCACAGGGATGGAAAGGATCACCAGCAATATTCAGAGTAGCATGAÇAAAAATCTT
AGAGCCCTTCAGAGCAAAAAATCCAGACATAGTTATCTATCAAGCCCCGTTGTATGTAGGATCTGACTTAGAAATAGGGC
AACATAGAGCAAAAAATAGAAGAGTTAAGGGAACATTTATTGAAATGGGGATTTACAACACCAGACAAGAAACATCAAAAA
GAACCCCCATTTCTTCCCATCGAATCCATCCTGACAAATGGACAGTACAACCTATACTGCTGCCAGAAAAGGATAGTTG
GACTGTCAATGATATACAGAAGTTAGTGGGAAAAATTAACTGGGCAAGTCAGATTTACCCAGGGATTAAAGTAAGGCAAC
TCTGTAAACTCCTCAGGGGGGCCAAAGCACTAACAGACATAGTACCCTAACTGAAGAAGCAGAATTAGAATTGGCAGAG
AACAGGGAAATTTTAAGAGAACCAGTACATGGAGTATATTATGATCCATCAAAAGACTTGATAGCTGAAATACAGAAACA
GGGGCATGAACAATGGACATATCAAATTTATCAAGAACCATTTAAAAATCTGAAAAACAGGGAAGTATGCAAAAAATGAGGA
CTACCCCACTAATGATGTAAACAGTTAACAGAGGCAGTGCAAAAAATAGCCATGGAAAGCATAGTAATATGGGGAAAG
ACTCCTAAATTTAGACTACCCATCCAAAAAGAAACATGGGAGACATGGTGGACAGACTATTGGCAAGCCACCTGGATCCC
TGAGTGGGAGTTTGTTAATACCCCTCCCCTAGTAAAATTATGGTACCAACTAGAAAAAGATCCCATAGCAGGAGTAGAAA
CTTTCTATGTAGATGGAGCAACTAATAGGGAAGCTAAAAATAGGAAAAGCAGGGTATGTTACTGACAGAGGAAGGCAGAAA
ATTGTTACTCTAACTAACACAACAATCAGAAGACTGAGTTACAAGCAATTCAGCTAGCTCTGCAGGATTCAGGATCAGA
AGTAAACATAGTAACAGACTCACAGTATGCATTAGGAATCATTCAAGCACAACCAGATAAGAGTGACTCAGAGATATTTA
ACCAAATAATAGAACAGTTAATAAACAAGGAAAGAATCTACCTGTCTGTTGGTACCAGCACATAAAGGAATTGGGGGAAAT
GAACAAGTAGATAAATTAGTAAGTAAGGGAATTAGGAAAGTGTTG

FIGURE 40

>ProtwtRTwt_TV1_C_ZAopt (SEQ ID NO:70)

CCCCAGATCACCTGTGGCAGCGCCCCCTGGTGAGCATCAAGGTGGAGGGCCAGATCAAGGAGGCCCTGCTGGACACCGG
CGCCGACGACACCGTGCTGGAGGAGATCGACCTGCCCCGGCAAGTGGAAGCCCAAGATGATCGGCGGCATCGGCGGCTTCA
TCAAGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAGGCCATCGGCACCGTGCTGGTGGGCCCCACC
CCCGTGAACATCATCGGCCGCAACCTGCTGACCCAGCTGGGCTGCACCCCTGAACTTCCCCATCAGCCCCATCGAGACCGT
GCCCCGTGAAGCTGAAGCCCCGGCATGGACGGCCCCAAGGTGAAGCAGTGGCCCCCTGACCGAGGAGAAGATCAAGGCCCTGA
CCGCCATCTGCGAGGAGATGGAGAAGGAGGGCAAGATCACCAAGATCGGCCCCGACAACCCCTACAACACCCCCGTGTTT
GCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGGACTTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTG
GGAGGTGCAGCTGGGCATCCCCACCCCGCCGGCCTGAAGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGGCGACGCCT
ACTTCAGCGTGCCCCCTGGACGAGAGCTTCCGCAAGTACACCGCCTTACCATCCCCAGCATCAACAACGAGACCCCCGGC
ATCCGCTACCAAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCAGCCCCGCCATCTTCCAGAGCAGCATGAACAAGATCCT
GGAGCCCTTCCGCGCCAAGAACCCCGACATCGTGATCTACCAAGTACATGGACGACCTGTACGTGGGCAGCGACCTGGAGA
TCGGCCAGCACCGCGCCAAGATCGAGGAGCTGCGCGAGCACCTGCTGAAGTGGGGCTTCAACACCCCGACAAGAAGCAC
CAGAAGGAGCCCCCTTCTGTGGATGGGCTACGAGCTGCACCCCGACAAGTGGACCGTGACGCCATCCTGCTGCCCCGA
GAAGGACAGCTGGACCGTGAACGACATCCAGAAGCTGGTGGGCAAGCTGAACTGGGCCAGCCAGATCTACCCCGGCATCA
AGGTGCGCCAGCTGTGCAAGCTGCTGCGCGCGCCAAGGCCCTGACCGACATCGTGCCCCTGACCGAGGAGGCCGAGCTG
GAGCTGGCCGAGAACC GCGAGATCCTGCGCGAGCCCGTGACGGCGTGTACTACGACCCAGCAAGGACCTGATCGCCGA
GATCCAGAAGCAGGGCCACGAGCAGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGACCGGCAAGTACG
CCAAGATGCGCACCAACCCACACCAACGACGTGAAGCAGCTGACCGAGGCCGTGAGAAGATCGCCATGGAGAGCATCGTG
ATCTGGGGCAAGACCCCAAGTTCCGCTGCCATCCAGAAGGAGACCTGGGAGACCTGGTGGACCGACTACTGGCAGGC
CACCTGGATCCCCGAGTGGGAGTTCTGTAACACCCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAAGGACCCCATCG
CCGGCGTGGAGACCTTCTACGTGGACGGCGCCACCAACCGCAGGCCAAGATCGGCAAGGCCGGCTACGTGACCGACCGC
GGCCGCCAGAAGATCGTGACCTGACCAACACCACCAACCGAAGACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGA
CAGCGGCAGCGAGGTGAACATCGTGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCAGCCGACAAGAGCGACA
GCGAGATCTTCAACCAGATCATCGAGCAGCTGATCAACAAGGAGCGCATCTACCTGAGCTGGGTGCCCCGCCACAAGGGC
ATCGGCGGCAACGAGCAGGTGGACAAGCTGGTGAGCAAGGGCATCCGCAAGGTGCTG

FIGURE 41

>ProtwtRTwt_TV1_C_ZAwT (SEQ ID NO:71)

CCTCAAATCACTCTTTGGCAGCGACCCCTTGTCTCAATAAAAGTAGAGGGCCAGATAAAGGAGGCTCTCTTAGACACAGG
AGCAGATGATACAGTATTAGAAGAAATAGATTTGCCAGGGAAATGGAAACCAAAATGATAGGGGGAATTGGAGGTTTTA
TCAAAGTAAGACAGTATGATCAAATACTTATAGAAATTTGTGGAAAAAGGCTATAGGTACAGTATTAGTAGGGCCTACA
CCAGTCAACATAAATTGGAAGAAATCTGTAACTCAGCTTGGATGCACACTAAATTTTCCAATTAGTCCTATTGAACTGT
ACCAGTAAATTTAAACCAGGAATGGATGGCCCCAAAGGTCAAACAATGGCCATTGACAGAAGAAAAATAAAAGCATTAA
CAGCAATTTGTGAGGAAATGGAGAAGGAAGGAAAAATTACAAAAATTTGGGCCTGATAATCCATATAAACTCCAGTATTT
GCCATAAAAAAGAAGGACAGTACTAAGTGGAGAAAAATTAGTAGATTTTCAGGGAACTCAATAAAAGAAGTCAAGACTTTTG
GGAAGTTCAATTAGGAATACCACACCCAGCAGGATTAAAAAGAAAAATCAGTGACAGTGCTAGATGTGGGGGATGCAT
ATTTTTTCAGTTCTTTAGATGAAAGCTTCAGGAAATATACTGCATTACCATACCTAGTATAAAACAATGAAACACCAGGG
ATTAGATATCAATATAATGTGCTGCCACAGGGATGGAAAGGATCACCAGCAATATTCAGAGTAGCATGA'AAAAATCTT
AGAGCCCTTCAGAGCAAAAAATCCAGACATAGTTATCTATCAATATATGGATGACTTGTATGTAGGATCTGACTTAGAAA
TAGGGCAACATAGAGCAAAAAATAGAAGAGTTAAGGGAACATTTATTGAAATGGGGATTTACAACACCAGACAAGAAACAT
CAAAAAGAACCCCCATTTCTTTGGATGGGGTATGAACTCCATCCTGACAAATGGACAGTACAACCTATACTGCTGCCAGA
AAAGGATAGTTGGACTGTCAATGATATACAGAAGTTAGTGGGAAAATTAACCTGGGCAAGTCAGATTTACCCAGGGATTA
AAGTAAGGCAACTCTGTAAACTCCTCAGGGGGGCCAAAGCACTAACAGACATAGTACCACTAACTGAAGAAGCAGAATTA
GAATTGGCAGAGAACAGGGAAATTTTAAGAGAACAGTACATGGAGTATATTATGATCCATCAAAAGACTTGATAGCTGA
AATACAGAAACAGGGGCATGAACAATGGACATATCAAATTTATCAAGAACCATTTAAAAATCTGAAAACAGGGAAGTATG
CAAAAAATGAGGACTACCCACACTAATGATGTAAACAGTTAACAGAGGCAGTGCAAAAAATAGCCATGGAAAGCATAGTA
ATATGGGGAAAGACTCCTAAATTTAGACTACCCATCCAAAAAGAAACATGGGAGACATGGTGGACAGACTATTGGCAAGC
CACCTGGATCCCTGAGTGGGAGTTTGTTAATACCCCTCCCCTAGTAAAATTATGGTACCAACTAGAAAAAGATCCCATAG
CAGGAGTAGAACTTTCTATGTAGATGGAGCAACTAATAGGGAAGCTAAAAATAGGAAAAGCAGGGTATGTTACTGACAGA
GGAAGGCAGAAAATTGTTACTCTAACTAACACAACAAATCAGAAGACTGAGTTACAAGCAATTCAGCTAGCTCTGCAGGA
TTCAGGATCAGAAGTAAACATAGTAACAGACTCACAGTATGCATTAGGAATCATTCAAGCACAACCAGATAAGAGTGACT
CAGAGATATTTAACCATAATAGAACAGTTAATAACAAGGAAAGAATCTACCTGTCTATGGGTACCAGCACATAAAGGA
ATTGGGGGAAATGAACAAGTAGATAAATTAGTAAGTAAGGGAATTAGGAAAGTGTTG

FIGURE 42

>RevExon1_TV1_C_ZAopt (SEQ ID NO:72)

ATGGCCGGCCGCAGCGGCGACAGCGACGAGGCCCTGCTGCAGGTGGTGAAGATCATCAAGATCCTGTACCAGAGC

FIGURE 43

FIGURE 43

>RevExon1_TV1_C_ZAw1 (SEQ ID NO:73)

ATGGCAGGAAGAAGCGGAGACAGCGACGAAGCGCTCCTCCAAGTGGTGAAGATCATCAAAATCCTCTATCAAAGCA

FIGURE 44

FIGURE 44

>RevExon2_TV1_C_ZAopt-2 (SEQ ID NO:74)

CCCTACCCCAAGCCCGAGGGCACCCGCCAGGCCCCGCCGCAACCGCCGCCGCTGGCGCGCCCGCCAGCGCCAGATCCA
CACCATCGGCGAGCGCATCCTGGTGGCCTGCCTGGGCCGCAGCGCCGAGCCCGTGCCCTGCAGCTGCCCCCCTGGAGC
GCCTGCACATCAACTGCAGCGAGGGCAGCGGCACCAGCGGCACCCAGCAGAGCCAGGGCACCACCGAGGGCGTGGGCGAC
CCCTAA

FIGURE 45

FIGURE 45

>RevExon2_TV1_C_ZAwT (SEQ ID NO:75)

ACCCTTACCCCAAGCCCGAGGGGACTCGACAGGCTCGGAGGAATCGAAGAAGAAGGTGGAGAGCAAGACAGAGACAGATC
CATACGATTGGTGAGCGGATTCTTGTCTGCTTGCCTGGGACGATCTGCGGAGCCTGTGCCTCTTCAGCTACCACCGCTTGA
GAGACTTCATATTAATTGCAGTGAGGGCAGTGGAACCTCTGGGACACAGCAGTCTCAGGGGACTACAGAGGGGGTGGGAG
ATCCTTAA

FIGURE 46

1050405256660

RT_TV1_C_ZAopt (SEQ ID NO:76)

CCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCATGGACGGCCCCA
AGGTGAAGCAGTGGCCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCGCCATCTGCG
AGGAGATGGAGAAGGAGGGCAAGATCACCAAGATCGGCCCCGACAACCCCTACAACA
CCCCCGTGTTCGCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGGACTT
CCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCCAC
CCCGCCGGCCTGAAGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGGCGACGCCTAC
TTCAGCGTGCCCTGGACGAGAGCTTCCGCAAGTACACCGCCTTCACCATCCCCAGCA
TCAACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAA
GGGCAGCCCCGCCATCTTCCAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCC
AAGAACCCCGACATCGTGATCTACCAGTACATGGACGACCTGTACGTGGGCAGCGACC
TGGAGATCGGCCAGCACCGCGCCAAGATCGAGGAGCTGCGCGAGCACCTGCTGAAGT
GGGGCTTCACCACCCCGACAAGAAGCACCAAGAAGGAGCCCCCTTCCTGTGGATGGG
CTACGAGCTGCACCCCGACAAGTGGACCGTGCAGCCCATCCTGCTGCCCCGAGAAGGAC
AGCTGGACCGTGAACGACATCCAGAAGCTGGTGGGCAAGCTGAACTGGGCCAGCCAG
ATCTACCCCGGCATCAAGGTGCGCCAGCTGTGCAAGCTGCTGCGCGGCGCCAAGGCCC
TGACCGACATCGTGCCCTGACCGAGGAGGCCGAGCTGGAGCTGGCCGAGAACCGCG
AGATCCTGCGCGAGCCCGTGACCGGCGTGTACTACGACCCAGCAAGGACCTGATCGC
CGAGATCCAGAAGCAGGGCCACGAGCAGTGGACCTACCAGATCTACCAGGAGCCCTT
CAAGAACCTGAAGACCGGCAAGTACGCCAAGATGCGCACCAACCCACACCAACGACGT
GAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCATGGAGAGCATCGTGATCTGGGG
CAAGACCCCAAGTTCCGCCTGCCCATCCAGAAGGAGACCTGGGAGACCTGGTGGACC
GACTACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTTCGTGAACACCCCCCCCCTGG
TGAAGCTGTGGTACCAGCTGGAGAAGGACCCCATCGCCGGCGTGGAGACCTTCTACGT
GGACGGCGCCACCAACCGCGAGGCCAAGATCGGCAAGGCCGGCTACGTGACCGACCG
CGGCCGCCAGAAGATCGTGACCCTGACCAACACCACCAACCAGAAGACCGAGCTGCA
GGCCATCCAGCTGGCCCTGCAGGACAGCGGCAGCGAGGTGAACATCGTGACCGACAG
CCAGTACGCCCTGGGCATCATCCAGGCCAGCCCGACAAGAGCGACAGCGAGATCTTC
AACCAGATCATCGAGCAGCTGATCAACAAGGAGCGCATCTACCTGAGCTGGGTGCCCG
CCCACAAGGGCATCGGCGGCAACGAGCAGGTGGACAAGCTGGTGAGCAAGGGCATCC
GCAAGGTGCTG

FIGURE 47

>RT_TV1_C_ZAwT (SEQ ID NO:77)

CCAATTAGTCCTATTGAAACTGTACCAGTAAAAATTAAACCAGGAATGGATGGCCCAAAGGTCAAACAATGGCCATTGAC
AGAAGAAAAAATAAAAGCATTAACAGCAATTTGTGAGGAAATGGAGAAGGAAGGAAAAATTACAAAAATTGGGCCTGATA
ATCCATATAACACTCCAGTATTTGCCATAAAAAAGAAGGACAGTACTAAGTGGAGAAAATTAGTAGATTTTCAGGGAACTC
AATAAAAGAACTCAAGACTTTTGGGAAGTTCAATTAGGAATACCACACCCAGCAGGATTAAAAAAGAAAAATCAGTGAC
AGTGCTAGATGTGGGGGATGCATATTTTTCAGTTCCTTTAGATGAAAGCTTCAGGAAATATACTGCATTACCCATACCTA
GTATAACAATGAAACACCAGGGATTAGATATCAATATAATGTGCTGCCACAGGGATGGAAAGGATCACCAGCAATATTC
CAGAGTAGCATGACAAAAATCTTAGAGCCCTTCAGAGCAAAAAATCCAGACATAGTTATCTATCAATATATGGATGACTT
GTATGTAGGATCTGACTTAGAAATAGGGCAACATAGAGCAAAAAATAGAAGAGTTAAGGGAACATTTATTGAAATGGGGAT
TTACAACACCAGACAAGAAACATCAAAAAAGAACCCCATTTCTTTGGATGGGGTATGAACTCCATCCTGACAAATGGACA
GTACAACCTATACTGCTGCCAGAAAAGGATAGTTGGACTGTCAATGATATACAGAAGTTAGTGGGAAAATTAACTGGGC
AAGTCAGATTTACCCAGGGATTAAAGTAAGGCAACTCTGTAACTCCTCAGGGGGGCCAAAGCACTAACAGACATAGTAC
CACTAACTGAAGAAGCAGAATTAGAATTGGCAGAGAACAGGGAAATTTTAAGAGAACCAGTACATGGAGTATATTATGAT
CCATCAAAAGACTTGATAGCTGAAATACAGAAACAGGGGCATGAACAATGGACATATCAAATTTATCAAGAACCATTAA
AAATCTGAAAACAGGGAAGTATGCAAAAAATGAGGACTACCCACACTAATGATGTAAAACAGTTAACAGAGGCAGTGCAAA
AAATAGCCATGGAAAGCATAGTAATATGGGGAAAGACTCCTAAATTTAGACTACCCATCCAAAAAGAAACATGGGAGACA
TGGTGGACAGACTATTGGCAAGCCACCTGGATCCCTGAGTGGGAGTTTGTTAATACCCCTCCCCTAGTAAATTTATGGTA
CCAACTAGAAAAAGATCCCATAGCAGGAGTAGAACTTTCTATGTAGATGGAGCAACTAATAGGGAAGCTAAAAATAGGAA
AAGCAGGGTATGTTACTGACAGAGGAAGGCAGAAAATTGTTACTCTAACTAACACAACAAATCAGAAGACTGAGTTACAA
GCAATTCAGCTAGCTCTGCAGGATTAGGATCAGAAGTAAACATAGTAACAGACTCACAGTATGCATTAGGAATCATTC
AGCACAACCAGATAAGAGTGACTCAGAGATATTTAACCAATAATAGAACAGTTAATAACAAGGAAAGAATCTACCTGT
CATGGGTACCAGCACATAAAGGAATTGGGGGAAATGAACAAGTAGATAAATTAGTAAGTAAGGGAATTAGGAAAGTGTG

FIGURE 48

FIGURE 48

>RTmut_TV1_C_ZAopt (SEQ ID NO:78)

CCCATCAGCCCCATCGAGACCGTGCCCGTGAAGCTGAAGCCCGGCATGGACGGCCCCAAGGTGAAGCAGTGGCCCCCTGAC
CGAGGAGAAGATCAAGGCCCTGACCGCCATCTGCGAGGAGATGGAGAAGGAGGGCAAGATCACCAAGATCGGCCCCGACA
ACCCCTACAACACCCCGTGTTTCGCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGGACTTCCGCGAGCTG
AACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCACCCCGCCGGCTGAAGAAGAAGAAGAGCGTGAC
CGTGCTGGACGTGGGCGACGCCTACTTCAGCGTGCCCTGGACGAGAGCTTCCGCAAGTACACCGCCTTCACCATCCCCA
GCATCAACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGGCAGCCCCGCCATCTTC
CAGAGCAGCATGACCAAGATCCTGGAGCCCTTCCGCGCCAAGAACCCCGACATCGTGATCTACCAGGCCCCCTGTACGT
GGGCAGCGACCTGGAGATCGGCCAGCACCGCGCCAAGATCGAGGAGCTGCGCGAGCACCTGCTGAAGTGGGGCTTCACCA
CCCCGACAAGAAGCACCAGAAGGAGCCCCCTTCTGCCCATCGAGCTGCACCCCGACAAGTGGACCGTGCAGCCCATC
CTGCTGCCCCGAGAAGGACAGCTGGACCGTGAACGACATCCAGAAGCTGGTGGGCAAGCTGAACTGGGCCAGCCAGATCTA
CCCCGGCATCAAGGTGCGCCAGCTGTGCAAGCTGTGCGCGCGCCAAGGCCCTGACCGACATCGTGCCCTGACCGAGG
AGGCCGAGCTGGAGCTGGCCGAGAACCGCGAGATCCTGCGCGAGCCCGTGCACGGCGTGTAACGACCCAGCAAGGAC
CTGATCGCCGAGATCCAGAAGCAGGGCCACGAGCAGTGGACCTACCAGATCTACCAGGAGCCCTTCAAGAACCTGAAGAC
CGGCAAGTACGCCAAGATGCGCACCAACCCACACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATCGCCATGG
AGAGCATCGTGATCTGGGGCAAGACCCCCAAGTTCCGCTGCCCATCCAGAAGGAGACCTGGGAGACCTGGTGGACCGAC
TACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTTCTGTAACACCCCCCCCCCTGGTGAAGCTGTGGTACCAGCTGGAGAA
GGACCCCATCGCCGGCGTGGAGACCTTCTACGTGGACGGCGCCACCAACCGCGAGGCCAAGATCGGCAAGGCCGGCTACG
TGACCGACCGCGGCCGCCAGAAGATCGTGACCCTGACCAACACCACCAACCAGAAGACCGAGCTGCAGGCCATCCAGCTG
GCCCTGCAGGACAGCGGCAGCGAGGTGAACATCGTGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCAGCCCCGA
CAAGAGCGACAGCGAGATCTTCAACCAGATCATCGAGCAGCTGATCAACAAGGAGCGCATCTACCTGAGCTGGGTGCCCG
CCCACAAGGGCATCGGCGCAACGAGCAGGTGGACAAGCTGGTGAGCAAGGGCATCCGCAAGGTGCTG

FIGURE 49

5256660

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FIGURE 50

>TatC22Exon1_TV1_C_ZAopt (SEQ ID NO:80)

ATGGAGCCCGTGGACCCCAAGCTGAAGCCCTGGAACCACCCCGGCAGCCAGCCCAAGACCGCCGGCAACAACCTGCTTCTG
CAAGCACTGCAGCTACCACTGCCTGGTGTGCTTCCAGACCAAGGGCCTGGGCATCAGCTACGGCCGCAAGAAGCGCCGCC
AGCGCCGCAGCGCCCCCCCCCAGCGGCGAGGACCACCAGAACCCCTGAGCAAGCAG

FIGURE 51

1030-52660

>TatExon1_TV1_C_ZAopt (SEQ ID NO:81)

ATGGAGCCCGTGGACCCCAAGCTGAAGCCCTGGAACCAACCCGGCAGCCAGCCCAAGACCGCCTGCAACAACCTGCTTCTG
CAAGCACTGCAGCTACCACTGCCTGGTGTGCTTCCAGACCAAGGGCCTGGGCATCAGCTACGGCCGCAAGAAGCGCCGCC
AGCGCCGCAGCGCCCCCCCCAGCGGCGAGGACCACCAGAACCCCTGAGCAAGCAG

FIGURE 52

FIGURE 52

>TatExon1_TV1_C_ZAw (SEQ ID NO:82)

ATGGAGCCAGTAGATCCTAAACTAAAGCCCTGGAACCATCCAGGAAGCCAACCTAAACAGCTTGTAATAATTGCTTTTG
CAAACACTGTAGCTATCATTGTCTAGTTTGCTTTTCAGACAAAAGGTTTAGGCATTTCTTATGGCAGGAAGAAGCGGAGAC
AGCGACGAAGCGCTCCTCCAAGTGGTGAAGATCATCAAATCCTCTATCAAAGCAG

FIGURE 53

Figure 53

>TatExon2_TV1_C_ZAopt (SEQ ID NO:83)

CCCCTGCCCCAGGCCCCGCGCGACAGCACCGGCAGCGAGGAGAGCAAGAAGAAGGTGGAGAGCAAGACCGAGACCGACCC
CTACGACTGGTGA

FIGURE 54

FIGURE 54

>TatExon2_TV1_C_ZAw1 (SEQ ID NO:84)

CCCTTACCCCAAGCCCGAGGGGACTCGACAGGCTCGGAGGAATCGAAGAAGAAGGTGGAGAGCAAGACAGAGACAGATCC
ATACGATTGGTGA

FIGURE 55

FIGURE 55

>Vif_TV1_C_ZAopt (SEQ ID NO:85)

ATGGAGAACCGCTGGCAGGTGCTGATCGTGTGGCAGGTGGACCGCATGAAGATCCGCGCCTGGAACAGCCTGGTGAAGCA
CCACATGTACATCAGCCGCCGCGCCAGCGGCTGGGTGTACCGCCACCACTTCGAGAGCCGCCACCCCAAGGTGAGCAGCG
AGGTGCACATCCCCCTGGGCGACGCCCCGCTGGTGATCAAGACCTACTGGGGCCTGCAGACCGGCGAGCGCGACTGGCAC
CTGGGCCACGGCGTGAGCATCGAGTGGCGCCTGCGCGAGTACAGCACCCAGGTGGACCCGACCTGGCCGACCAGCTGAT
CCACATGCACTACTTCGACTGCTTCACCGAGAGCGCCATCCGCCAGGCCATCCTGGGCCACATCGTGTTCCCCCGCTGCG
ACTACCAGGCCGCCACAAGAAGGTGGGCAGCCTGCAGTACCTGGCCCTGACCGCCCTGATCAAGCCCAAGAAGCGCAAG
CCCCCCTGCCCAGCGTGCGCAAGCTGGTGGAGGACCGCTGGAACGACCCCAGAAGACCCGCGGCCGCGCGCAACCA
CACCATGAACGGCCACTAG

FIGURE 56

FIGURE 56

[illegible]

FIGURE 57

>Vpr_TV1_C_ZAopt (SEQ ID NO:87)

ATGGAGCGCCCCCGAGGACCAGGGCCCCCAGCGCGAGCCCTACAACGAGTGGACCCTGGAGATCCTGGAGGAGCTGAA
GCAGGAGGCCGTGCGCCACTTCCCCCGCCCCTGGCTGCACAGCCTGGGCCAGTACATCTACGAGACCTACGGCGACACCT
GGACCGGCGTGGAGGCCATCATCCGCGTGCTGCAGCAGCTGCTGTTCATCCACTTCCGCATCGGCTGCCAGCACAGCCGC
ATCGGCATCCTGCGCCAGCGCCGCGCCCGCAACGGCGCCAGCCGCAGC

FIGURE 58

FIG. 58 "5256660

>Vpr_TV1_C_ZAwT (SEQ ID NO:88)

ATGGAACGACCCCCAGAAGACCAGGGGCCGCAGAGGGAACCATACAATGAATGGACACTAGAGATTCTAGAAGAACTCAA
GCAGGAAGCTGTCAGACACTTTCCTAGACCATGGCTCCATAGCTTAGGACAATATATCTATGAAACCTATGGGGATACTT
GGACGGGAGTTGAAGCTATAATAAGAGTACTGCAACAACACTACTGTTTCATTTCAGAAATTGGATGCCAACATAGCAGA
ATAGGCATCTTGCGACAGAGAAGAGCAAGAAATGGAGCCAGTAGATCC

FIGURE 59

105020"52565350

>Vpu_TV1_C_ZAopt (SEQ ID NO:89)

ATGGTGAGCCTGAGCCTGTTCAAGGGCGTGGACTACCGCCTGGGCGTGGGCGCCCTGATCGTGGCCCTGATCATCGCCAT
CATCGTGTGGACCATCGCCTACATCGAGTACCGCAAGCTGGTGCGCCAGAAGAAGATCGACTGGCTGATCAAGCGCATCC
GCGAGCGCGCCGAGGACAGCGGCAACGAGAGCGACGGCGACACCGAGGAGCTGAGCACCATGGTGGACATGGGCCACCTG
CGCCTGCTGGACGCCAACGACCTGTAA

FIGURE 60

FIGURE 60

>Vpu_TV1_C_ZAwT (SEQ ID NO:90)

ATGGTAAGTTTAAGTTTATTTAAAGGAGTAGATTATAGATTAGGAGTAGGAGCATTGATAGTAGCACTAATCATAGCAAT
AATAGTGTGGACCATAGCATATATAGAATATAGGAAATTGGTAAGACAAAAGAAAATAGACTGGTTAATTAAAAGAATTA
GGGAAAGAGCAGAAGACAGTGGCAATGAGAGTGATGGGGACACAGAAGAATTGTCAACAATGGTGGATATGGGGCATCTT
AGGCTTCTGGATGCTAATGATTGTAA

FIGURE 61

090915-070501

dna revexon1_2TV1_C_ZAop (SEQ ID NO:91)

ATGGCCGGCCGCAGCGGCGACAGCGACGAGGCCCTGCTGCAGGTGGTGAAGATCATC
AAGATCCTGTACCAGAGCCCCTACCCCAAGCCCGAGGGCACCCGCCAGGCCCGCCGCA
ACCGCCGCCGCCGCTGGCGCGCCCGCCAGCGCCAGATCCACACCATCGGCGAGCGCAT
CCTGGTGGCCTGCCTGGGCGCGAGCGCCGAGCCCGTGCCCCTGCAGCTGCCCCCCTG
GAGCGCCTGCACATCAACTGCAGCGAGGGCAGCGGCACCAGCGGCACCCAGCAGAGC
CAGGGCACCAACGAGGGCGTGGGCGACCCCTAA

FIGURE 62

FIGURE 62

dna Revexon1_2_TV1_C_ZAwt (SEQ ID NO:92)

ATGGCAGGAAGAAGCGGAGACAGCGACGAAGCGCTCCTCCAAGTGGTGAAGATCATC
AAAATCCTCTATCAAAGCAACCCTTACCCCAAGCCCGAGGGGACTCGACAGGCTCGGA
GGAATCGAAGAAGAAGGTGGAGAGCAAGACAGAGACAGATCCATACGATTGGTGAGC
GGATTCTTGTGCGCTTGCCTGGGACGATCTGCGGAGCCTGTGCCTCTTCAGCTACCACCG
CTTGAGAGACTTCATATTAATTGCAGTGAGGGCAGTGGAAGTTCTGGGACACAGCAGT
CTCAGGGGACTACAGAGGGGGGTGGGAGATCCTTAA

FIGURE 63

FIGURE 63

dna TatC22Exon1_2_TV1_C_ZAopt (SEQ ID NO:93)

ATGGAGCCCGTGGACCCCAAGCTGAAGCCCTGGAACCAACCCCGGCAGCCAGCCCAAG
ACCGCCGGCAACAACCTGCTTCTGCAAGCACTGCAGCTACCACTGCCTGGTGTGCTTCC
AGACCAAGGGCCTGGGCATCAGCTACGGCCGCAAGAAGCGCCGCCAGCGCCGCAGCG
CCCCCCCCAGCGGCGAGGACCACCAGAACCCCTGAGCAAGCAGCCCCTGCCCCAGGC
CCGCGGCGACAGCACCGGCAGCGAGGAGAGCAAGAAGAAGGTGGAGAGCAAGACCG
AGACCGACCCCTACGACTGGTGA

FIGURE 64

FIGURE 64

dna TatExon1_2_TV1_C_ZAopt (SEQ ID NO:94)

ATGGAGCCCGTGGACCCCAAGCTGAAGCCCTGGAACCACCCCGGCAGCCAGCCCAAG
ACCGCCTGCAACAAGTCTTCTGCAAGCACTGCAGCTACCACTGCCTGGTGTGCTTCCA
GACCAAGGGCCTGGGCATCAGCTACGGCCGCAAGAAGCGCCGCAGCGCCGCAGCGCC
CCCCCAGCGGCGAGGACCACAGAACCCCTGAGCAAGCAGCCCCTGCCCCAGGCCC
GCGGCGACAGCACCGGCAGCGAGGAGAGCAAGAAGAAGGTGGAGAGCAAGACCGAG
ACCGACCCCTACGACTGGTGA

FIGURE 65

705020 5456850

dna TatExon1_2_TV1_C_ZAwt (SEQ ID NO:95)

ATGGAGCCAGTAGATCCTAAACTAAAGCCCTGGAACCATCCAGGAAGCCAACCTAAA
ACAGCTTGTAATAATTGCTTTTGCAAACACTGTAGCTATCATTGTCTAGTTTGCTTTCA
GACAAAAGGTTTAGGCATTCCTATGGCAGGAAGAAGCGGAGACAGCGACGAAGCGC
TCCTCCAAGTGGTGAAGATCATCAAAATCCTCTATCAAAGCAGCCCTTACCCCAAGCC
CGAGGGGACTCGACAGGCTCGGAGGAATCGAAGAAGAAGGTGGAGAGCAAGACAGA
GACAGATCCATACGATTGGTGA

FIGURE 66

0999575-070504

NefD125G-Myr_TV1_C_ZAopt (SEQ ID NO:96)

ATGGCCGGCAAGTGGAGCAAGCGCAGCATCGTGGGCTGGCCCCGCGTGCGC
GAGCGCATGCGCCGCACCGAGCCCGCCGCCGAGGGCGTGGGCGCCGCCAGC
CAGGACCTGGACCGCCACGGCGCCCTGACCAGCAGCAACACCCCCGCCACCA
ACGAGGCCTGCGCCTGGCTGCAGGCCCCAGGAGGAGGACGGCGACGTGGGCT
TCCCCGTGCGCCCCCAGGTGCCCCCTGCGCCCCATGACCTACAAGAGCGCCGT
GGACCTGAGCTTCTTCCTGAAGGAGAAGGGCGGCCTGGAGGGCCTGATCTAC
AGCCGCAAGCGCCAGGAGATCCTGGACCTGTGGGTGTACAACACCCAGGGCT
TCTTCCCCGGCTGGCAGAACTACACCAGCGGCCCCGGCGTGCGCTTCCCCCTG
ACCTTCGGCTGGTGCTTCAAGCTGGTGCCCCGTGGACCCCCGCGAGGTGAAGG
AGGCCAACGAGGGCGAGGACAACCTGCCTGCTGCACCCCATGAGCCAGCACG
GCGCCGAGGACGAGGACCGCGAGGTGCTGAAGTGGAAGTTCGACAGCCTGC
TGGCCCACCGCCACATGGCCCCGCGAGCTGCACCCCGAGTACTACAAGGACTG
CTGA

FIGURE 67

105020" 5256680

ATGCGCGCCCGCGGCATCCTGAAGAACTACCGCCACTGGTGGATCTGGGGCATCCT
 GGGCTTCTGGATGCTGATGATGTGCAACGTGAAGGGCCTGTGGGTGACCGTGTACTA
 CGGCGTGCCCGTGGGGCCGCGAGGCCAAGACCACCTGTTCTGCGCCAGCGACGCCA
 AGGCCTACGAGAAGGAGGTGCACAACGTGTGGGGCCACCCACGCCTGCGTGCCCAAC
 GACCCCAACCCCCAGGAGGTGATCCTGGGCAACGTGACCGAGAAGTTCAACATGTG
 GAAGAACGACATGGTGGACCAGATGCAGGAGGACATCATCAGCCTGTGGGACCAGA
 GCCTGAAGCCCTGCGTGAAGCTGACCCCCCTGTGCGTGACCCTGAACTGCACCAACG
 CCACCGTGAAGTACAACAACACCAGCAAGGACATGAAGAACTGCAGCTTCTACGTG
 ACCACCGAGCTGCGCGACAAGAAGAAGAAGGAGAACGCCCTGTTCTACCGCCTGGA
 CATCGTGCCCTGAACAACCGCAAGAACGGCAACATCAACAACCTACCGCCTGATCA
 ACTGCAACACCAGCGCCATCACCCAGGCCTGCCCCAAGGTGAGCTTCGACCCCATCC
 CCATCCACTACTGCGCCCCCGCCGGCTACGCCCCCTGAAGTGCAACAACAAGAAG
 TTCAACGGCATCGGCCCTGCGACAACGTGAGCACCGTGCAGTGCACCCACGGCAT
 CAAGCCCGTGGTGAGCACCCAGCTGCTGCTGAACGGCAGCCTGGCCGAGGAGGAGA
 TCATCATCCGCAGCGAGAACCTGACCAACAACGTGAAGACCATCATCGTGACCTG
 AACGAGAGCATCGAGATCAAGTGACCCGCCCCGGCAACAACACCCGCAAGAGCGT
 GCGCATCGGCCCGGCCAGGCCTTCTACGCCACCGGCGACATCATCGGCGACATCC
 GCCAGGCCCACTGCAACATCAGCAAGAACGAGTGGAACACCACCCTGCAGCGCGTG
 AGCCAGAAGCTGCAGGAGCTGTTCCCCAACAGCACCGGCATCAAGTTCGCCCCCA
 CAGCGGCGGCGACCTGGAGATCACCAACCCACAGCTTCAACTGCGGCGGCGAGTTCT
 TCTACTGCAACACCACCGACCTGTTCAACAGCACCTACAGCAACGGCACCTGCACCA
 ACGGCACCTGCATGAGCAACAACACCGAGCGCATCACCTGCAGTGCCGCATCAAG
 CAGATCATCAACATGTGGCAGGAGGTGGGCCGCGCCATGTACGCCCCCCCCATCGC
 CGGCAACATCACCTGCCGAGCAACATCACCGGCCTGCTGCTGACCCGCGACGGCG
 GCGACAACAACACCGAGACCGAGACCTTCCGCCCCGGCGGCGGCGACATGCGCGAC
 AACTGGCGCAGCGAGCTGTACAAGTACAAGGTGGTGGAGATCAAGCCCCCTGGGCGT
 GGCCCCCACCGCCGCCAAGCGCCGCGTGGTGGAGCGCGAGAAGCGCGCCGTGGGCA
 TCGGCGCCGTGTTCTTGGGCTTCTTGGGCGCCGCCGCGCAGCACCATGGGCGCCGCCA
 GCATCACCTGACCGTGCAGGCCCGCCAGCTGCTGAGCGGCATCGTGCAGCAGCAG
 AGCAACCTGCTGCGCGCCATCGAGGCCCAGCAGCACATGCTGCAGCTGACCGTGTG
 GGGCATCAAGCAGCTGCAGGCCCGCGTGCTGGCCATCGAGCGCTACCTGCAGGACC
 AGCAGCTGCTGGGCCTGTGGGGCTGCAGCGGCAAGCTGATCTGCACCACCAACGTG
 CTGTGGAACAGCAGCTGGAGCAACAAGACCCAGAGCGACATCTGGGACAACATGAC
 CTGGATGCAGTGGGACCGCGAGATCAGCAACTACACCAACACCATCTACCGCCTGC
 TGGAGGACAGCCAGAGCCAGCAGGAGCGCAACGAGAAGGACCTGCTGGCCCTGGA
 CCGCTGGAACAACCTGTGGAAGTGGTTCAGCATCACCAACTGGCTGTGGTACATCAA
 GATCTTCATCATGATCGTGGGCGGCCTGATCGGCCTGCGCATCATCTTCGCCGTGCT
 GAGCCTGGTGAACCGCGTGCGCCAGGGCTACAGCCCCCTGAGCCTGCAGACCCTGA
 TCCCCAACCCCCGCGGCCCGACCGCCTGGGCGGCATCGAGGAGGAGGGCGGCGAG
 CAGGACAGCAGCCGAGCATCCGCCTGGTGAGCGGCTTCTGACCCTGGCCTGGGA
 CGACCTGCGCAGCCTGTGCCTGTTCTGCTACCACCGCCTGCGCGACTTCATCCTGAT
 CGTGGTGCAGCGCCGTGGAGCTGCTGGGCCACAGCAGCCTGCGCGGCCTGCAGCGCG
 GCTGGGGCACCTGAAGTACCTGGGCAGCCTGGTGCAGTACTGGGGCCTGGAGCTG
 AAGAAGAGCGCCATCAACCTGCTGGACACCATCGCCATCGCCGTGGCCGAGGGCAC
 CGACCGCATCCTGGAGTTCATCCAGAACCTGTGCCGCGGCATCCGCAACGTGCCCCG
 CCGCATCCGCCAGGGCTTCGAGGGCCGCCCTGCAGTAA

FIGURE 68

ATGAGAGCGAGGGGGATACTGAAGAATTATCGACACTGGTGGATATGGGGCATCTT
 AGGCTTTTGGATGCTAATGATGTGTAATGTGAAGGGCTTGTGGGTCACAGTCTACTA
 CGGGGTACCTGTGGGGAGAGAAGCAAAACTACTCTATTTTGTGCATCAGATGCTA
 AAGCATATGAGAAAGAAGTGCATAATGTCTGGGCTACACATGCCTGTGTACCCACA
 GACCCCAACCCACAAGAAGTGATTTTGGGCAATGTAACAGAAAATTTTAACATGTG
 GAAAAATGACATGGTGGATCAGATGCAGGAAGATATAATCAGTTTATGGGATCAAA
 GCCTTAAGCCATGTGTAAAATTGACCCCACTCTGTGTCACTTTAACTGTACAAATG
 CAACTGTAACTACAATAATACCTCTAAAGACATGAAAAATTGCTCTTTCTATGTAA
 CCACAGAATTAAGAGATAAGAAAAAGAAAGAAAATGCACTTTTTTATAGAÇTTGAT
 ATAGTACCACTTAATAATAGGAAGAATGGGAATATTAACAACCTATAGATTAATAAA
 TTGTAATACCTCAGCCATAACACAAGCCTGTCCAAAAGTCTCGTTTGACCCAATTCC
 TATACATTATTGTGCTCCAGCTGGTTATGCGCCTCTAAAATGTAATAATAAGAAATT
 CAATGGAATAGGACCATGCGATAATGTCAGCACAGTACAATGTACACATGGAATTA
 AGCCAGTGGTATCAACTCAATTACTGTAAATGGTAGCCTAGCAGAAGAAGAGATA
 ATAATTAGATCTGAAAATCTGACAAACAATGTCAAAACAATAATAGTACATCTTAAT
 GAATCTATAGAGATTAAATGTACAAGACCTGGCAATAATACAAGAAAGAGTGTGAG
 AATAGGACCAGGACAAGCATTCTATGCAACAGGAGACATAATAGGAGATATAAGAC
 AAGCACATTGTAACATTAGTAAAAATGAATGGAATACAACCTTTACAAAGGGTAAGT
 CAAAAATTACAAGAACTCTTCCCTAATAGTACAGGGATAAAAATTTGCACCACACTCA
 GGAGGGGACCTAGAAATTACTACACATAGCTTTAATTGTGGAGGAGAATTTTTCTAT
 TGCAATACAACAGACCTGTTTAATAGTACATACAGTAATGGTACATGCACTAATGGT
 ACATGCATGTCTAATAATACAGAGCGCATCACACTCCAATGCAGAATAAAACAAAT
 TATAAACATGTGGCAGGAGGTAGGACGAGCAATGTATGCCCCTCCCATTGCAGGAA
 ACATAACATGTAGATCAAATATTACAGGACTACTATTAACACGTGATGGAGGAGAT
 AATAATACTGAAACAGAGACATTCAGACCTGGAGGAGGAGACATGAGGGACAATTG
 GAGAAGTGAATTATATAAATACAAGGTGGTAGAAATTAAACCATTAGGAGTAGCAC
 CCACTGCTGCAAAAAGGAGAGTGGTGGAGAGAGAAAAAAGAGCAGTAGGAATAGG
 AGCTGTGTTTCTTGGGTTCTTGGGAGCAGCAGGAAGCACTATGGGCGCAGCATCAAT
 AACGCTGACGGTACAGGCCAGACAATTATTGTCTGGTATAGTGCAACAGCAAAGTA
 ATTTGCTGAGGGCTATAGAGGGCGCAACAGCATATGTTGCAACTCACGGTCTGGGGC
 ATTAAGCAGCTCCAGGCAAGAGTCCTGGCTATAGAGAGATACCTACAGGATCAACA
 GCTCCTAGGACTGTGGGGCTGCTCTGGAAAACCTCATCTGCACCACTAATGTGCTTTG
 GAACTCTAGTTGGAGTAATAAACTCAAAGTGATATTTGGGATAACATGACCTGGAT
 GCAGTGGGATAGGGAAATTAGTAATTACACAAACACAATATACAGGTTGCTTGAAG
 ACTCGCAAAGCCAGCAGGAAAGAAATGAAAAAGATTTACTAGCATTGGACAGGTGG
 AACAATCTGTGGAATTGGTTTAGCATAACAAATTGGCTGTGGTATATAAAAAATATTC
 ATAATGATAGTAGGAGGCTTGATAGGTTTAAGAATAATTTTTGCTGTGCTCTCTCTA
 GTAAATAGAGTTAGGCAGGGATACTCACCTTGTCAATTGCAGACCCTTATCCCAAAC
 CCGAGGGGACCCGACAGGCTCGGAGGAATCGAAGAAGAAGGTGGAGAGCAAGACA
 GCAGCAGATCCATTGATTAGTGAGCGGATTCTTGACACTTGCCTGGGACGACCTAC
 GAAGCCTGTGCCTCTTCTGCTACCACCGATTGAGAGACTTCATATTAATTGTAGTGA
 GAGCAGTGGAACCTTCTGGGACACAGTAGTCTCAGGGGACTGCAGAGGGGGTGGGGA
 ACCCTTAAGTATTTGGGGAGTCTTGTGCAATATTGGGGTCTAGAGTTAAAAAAGAGT
 GCTATTAATCTGCTTGATACTATAGCAATAGCAGTAGCTGAAGGAACAGATAGGATT
 CTAGAATTCATACAAAACCTTTGTAGAGGTATCCGCAACGTACCTAGAAGAATAAG
 ACAGGGCTTCGAAGCAGCTTTGCAATAA

TCGTCCTTGGGTTCTTGGGAGCAGCAGGAAGCACTATGGGCGCAGCATCAAT

FIGURE 69

Gag_TV2_C_ZAopt (SEQ ID NO:99)

ATGGGCGCCCGCGCCAGCATCCTGCGCGGGCGGCAAGCTGGACAAGTGGGAG
AAGATCCGCCTGCGCCCCGGCGGGCCGCAAGCACTACATGCTGAAGCACCTGG
TGTGGGCCAGCCGCGAGCTGGAGCGCTTCGCCGTGAACCCCGGCCTGCTGGA
GACCAGCGACGGCTGCCGCCAGATCATCAAGCAGCTGCAGCCCGCCCTGCAG
ACCGGCACCGAGGAGATCCGCAGCCTGTTCAACACCGTGGCCACCCTGTACT
GCGTGCACAAGGGCATCGACGTGCGCGACACCAAGGAGGGCCCTGGACAAGA
TCGAGGAGGAGCAGAACAAGTGCCAGCAGAAGACCCAGCAGGCCGAGGCCG
CCGACAAGAAGGTGAGCCAGAACTACCCCATCGTGCAGAACCTGCAGGGCC
AGATGGTGCACCAGGCCATCAGCCCCCGCACCCCTGAACGCCTGGGTGAAGGT
GATCGAGGAGAAGGCCTTCAGCCCCGAGGTGATCCCCATGTTACCCGCCCTG
AGCGAGGGCGCCACCCCCCAGGACCTGAACACCATGCTGAACACCGTGGGC
GGCCACCAGGCCGCCATGCAGATGCTGAAGGACACCATCAACGAGGAGGCC
GCCGAGTGGGACCGCCTGCACCCCGTGCACGCCGGCCCCCGTGGCCCCCGGCC
AGATGCGCGAGCCCCGCGGCAGCGACATCGCCGGCACCCAGCACCCCTGCA
GGAGCAGATCGCCTGGATGACCAGCAACCCCCCATCCCCGTGGGCGACATC
TACAAGCGCTGGATCATCCTGGGCCTGAACAAGATCGTGCGCATGTACAGCC
CCGTGAGCATCCTGGACATCAAGCAGGGCCCCAAGGAGCCCTTCCGCGACTA
CGTGGACCGCTTCTTCAAGACCCTGCGCGCCGAGCAGAGCACCCAGGAGGTG
AAGAACTGGATGACCGACACCCTGCTGGTGCAGAACGCCAACCCCGACTGCA
AGACCATCCTGCGCGCCCTGGGCCCCGGCGCCAGCCTGGAGGAGATGATGAC
CGCCTGCCAGGGCGTGGGCGGCCCCAGCCACAAGGCCCGCGTGCTGGCCGAG
GCCATGAGCCAGGCCAACAACACCAGCGTGATGATCCAGAAGAGCAACTTC
AAGGGCCCCCGCCGCGCCGTGAAGTGCTTCAACTGCGGCCGCGAGGGCCACA
TCGCCCCGCAACTGCCGCGCCCCCGCAAGCGCGGCTGCTGGAAGTGCGGCAA
GGAGGGCCACCAGATGAAGGACTGCACCGAGCGCCAGGCCAACTTCCTGGG
CAAGATCTGGCCAGCCACAAGGGCCGCCCCGGCAACTTCCTGCAGAGCCGC
CCCGAGCCCACCGCCCCCCCCCTGGAGCCACCGCCCCCCCCCGCCGAGAGCT
TCAAGTTCAAGGAGACCCCCAAGCAGGAGCCCAAGGACCGCGAGCCCCTGA
CCAGCCTGAAGAGCCTGTTCGGCAGCGACCCCCTGAGCCAGTAA

FIGURE 70

Gag_TV2_C_ZAwt (SEQ ID NO:100)

ATGGGTGCGAGAGCGTCAATATTAAGAGGGGGAAAATTAGACAAATGGGAA
AAAATTAGGTTACGGCCAGGGGGGAGAAAACACTATATGCTAAAACACCTA
GTATGGGCAAGCAGAGAGCTGGAAAGATTTGCAGTTAACCCTGGCCTTTTAG
AGACATCAGACGGATGTAGACAAATAATAAAACAGCTACAACCAGCTCTTCA
GACAGGAACAGAGGAAATTAGATCATTATTTAACACAGTAGCAACTCTCTAT
TGTGTACATAAAGGGATAGATGTACGAGACACCAAGGAAGCCTTAGACAAG
ATAGAGGAGGAACAAAACAAATGTCAGCAAAAAACACAGCAGGCGGAAGCG
GCTGACAAAAAGGTCAGTCAAAATTATCCTATAGTGCAGAACCTCCAAGGGC
AAATGGTACACCAGGCCATATCACCTAGAACCCTTGAATGCATGGGTAAAAGT
AATAGAGGAGAAGGCTTTTAGCCCAGAGGTAATACCCATGTTTACAGCATT
TCAGAAGGAGCCACCCACAAGATTTAAACACCATGTTAAATACAGTGGGGG
GACATCAAGCAGCCATGCAAATGTTAAAAGATACCATCAATGAGGAGGCTGC
AGAATGGGATAGGTTACATCCAGTACATGCAGGGCCTGTTGCACCAGGCCAG
ATGAGAGAACCAAGGGGAAGTGACATAGCAGGAACACTAGTACCCTTCAA
GAACAAATAGCATGGATGACAAGTAACCCACCTATCCCAGTAGGGGACATCT
ATAAAAGGTGGATAATTCTGGGGTTAAATAAAATAGTAAGAATGTACAGCCC
TGTCAGCATTTTAGACATAAAACAAGGACCAAAGGAACCCTTTAGAGACTAT
GTAGACCGGTTCTTCAAACTTTAAGAGCTGAACAATCTACAACAAGAGGTAA
AAAATTGGATGACAGACACCTTGTTAGTCCAAAATGCGAACCCAGATTGTAA
GACCATTTTAAGAGCATTAGGACCAGGGGCTTCATTAGAAGAAATGATGACA
GCATGTCAGGGAGTGGGAGGACCTAGCCACAAAGCAAGAGTTTTGGCTGAG
GCAATGAGCCAAGCAAACAATAACAAGTGTAATGATACAGAAAAGCAATTTTA
AAGGCCCTAGAAGAGCTGTTAAATGTTTCAACTGTGGCAGGGAAGGGCACAT
AGCCAGGAATTGCAGGGCCCCCTAGGAAAAGGGGCTGTTGGAAATGTGGAAA
GGAAGGACACCAAATGAAAGACTGTACTGAGAGGCAGGCTAATTTTTTAGGG
AAAATTTGGCCTTCCACAAGGGGAGGCCAGGGAATTCCTTCAGAGCAGAC
CAGAGCCAACAGCCCCACCACTAGAACCAACAGCCCCACCAGCAGAGAGCT
TCAAGTTCAAGGAGACTCCGAAGCAGGAGCCGAAAGACAGGGAACCTTTAA
CTTCCCTCAAATCACTCTTTGGCAGCGACCCCTTGTCTCAATAA

FIGURE 71

Nef_TV2_C_ZAopt (SEQ ID NO:101)

ATGGGCGGCAAGTGGAGCAAGAGCAGCATCATCGGCTGGCCCGAGGTGCGC
GAGCGCATCCGCCGCACCCGCAGCGCCGCCGAGGGCGTGGGCAGCGCCAGC
CAGGACCTGGAGAAGCACGGCGCCCTGACCACCAGCAACACCGCCCACAAC
AACGCCGCCTGCGCCTGGCTGGAGGCCCAGGAGGAGGAGGGCGAGGTGGGC
TTCCCCGTGCGCCCCCAGGTGCCCCCTGCGCCCCATGACCTACAAGGCCGCCAT
CGACCTGAGCTTCTTCTGAAGGAGAAGGGCGGCCTGGAGGGCCTGATCTAC
AGCAAGAAGCGCCAGGAGATCCTGGACCTGTGGGTGTACAACACCCAGGGC
TTCTTCCCGACTGGCAGAACTACACCCCGGCCCGGCGTGCGCTTCCCCCT
GACCTTCGGCTGGTACTTCAAGCTGGAGCCCGTGGACCCCGCGAGGTGGAG
GAGGCCAACGAGGGCGAGAACAACCTGCCTGCTGCACCCCATGAGCCAGCAC
GGCATGGAGGACGAGGACCGCGAGGTGCTGCGCTGGAAGTTCGACAGCACC
CTGGCCCGCCGCCACATGGCCCGCGAGCTGCACCCCGAGTACTACAAGGACT
GCTGA

FIGURE 72

105040-5256860

Nef_TV2_C_ZAw1 (SEQ ID NO:102)

ATGGGGGGCAAGTGGTCAAAAAGCAGTATAATTGGATGGCCTGAAGTAAGA
GAAAGAATCAGACGAACTAGGTCAGCAGCAGAGGGAGTAGGATCAGCGTCT
CAAGACTTAGAGAAACATGGGGCACTTACAACCAGCAACACAGCCCACAAC
AATGCTGCTTGCGCCTGGCTGGAAGCGCAAGAGGAGGAAGGAGAAGTAGGC
TTTCCAGTCAGACCTCAGGTACCTTTAAGACCAATGACTTATAAAGCAGCAAT
AGATCTCAGCTTCTTTTTAAAAGAAAAGGGGGGACTGGAAGGGTTAATTTAC
TCCAAGAAAAGGCAAGAGATCCTTGATTTGTGGGTTTATAACACACAAGGCT
TCTTCCCTGATTGGCAAACTACACACCGGGACCAGGGGTCAGATTTCCACT
GACCTTTGGATGGTACTTCAAGCTAGAGCCAGTCGATCCAAGGGAAGTAGAA
GAGGCCAATGAAGGAGAAAACAACCTGTTTACTACACCCTATGAGCCAGCATG
GAATGGAGGATGAAGACAGAGAAGTATTAAGATGGAAGTTTGACAGTACGC
TAGCACGCAGACACATGGCCCGCGAGCTACATCCGGAGTATTACAAAGACTG
CTGA

FIGURE 73

FIGURE 73

TTCTTCCGCGAGAACCTGGCCTTCCCCAGGGCGAGGCCCGCGAGTTCCCCAGCGAGCAGACC
CGCGCCAACAGCCCCACCACCCGCACCAACAGCCCCACCAGCCGCGAGCTGCAGGTGCAGGG
CGACAGCGAGGCCGGCGCCGAGCGCCAGGGCACCTTCAACTTCCCCCAGATCACCTGTGGC
AGCGCCCCCTGGTGAGCATCAAGGTGGCCGGCCAGACCAAGGAGGCCCTGCTGGACACCGGC
GCCGACGACACCGTGCTGGAGGAGATCAACCTGCCCGGCAAGTGGAAGCCCAAGATGATCGG
CGGCATCGGCGGCTTCATCAAGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCA
AGCGCGCCATCGGCACCGTGCTGGTGGGCCCCACCCCGTGAACATCATCGGCCGCAACCTGC
TGACCCAGCTGGGCTGCACCTGAACCTTCCCCATCAGCCCCATCGAGACCGTGCCCGTGAAGC
TGAAGCCCCGGCATGGACGGCCCCAAGGTGAAGCAGTGGCCCTGACCGAGGAGAAGATCAAG
GCCCTGACCGAGATCTGCGAGGAGATGGAGAAGGAGGGCAAGATCACCAAGATCGGCCCCG
AGAACCCCTACAACACCCCGTGTTCCGCCATCAAGAAGAAGGACAGCACCAAGTGCGCGAAG
CTGGTGGACTTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCAT
CCCCACCCCGCCGGCCTGAAGAAGAAGAAGAGCGTGACCGTGCTGGACGTGGGCGACGCCT
ACTTCAGCTGCCCCTGACGAGAGCTTCCGCAAGTACACCGCCTTACCATCCCCAGCATCA
ACAACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCCAGGGCTGGAAGGCGAGC
CCCGCCATCTTCCAGAGCAGCATGACCCGCATCCTGGAGCCCTTCCGCACCCAGAACCCCGAG
GTGGTGATCTACCAGTACATGGACGACCTGTACGTGGGCAGCGACCTGGAGATCGGCCAGCA
CCGCGCCAAGATCGAGGAGCTGCGCGGCCACCTGCTGAAGTGGGGCTTACCACCCCCGACA
AGAAGCACCAGAAGGAGCCCCCTTCTGTGGATGGGCTACGAGCTGCACCCCGACAAGTGG
ACCGTGACGCCATCCAGCTGCCCCGAGAAGGAGAGCTGGACCGTGAACGACATCCAGAAGCT
GGTGGGCAAGCTGAACCTGGGCCAGCCAGATCTACCCCGCATCAAGGTGCGCCAGCTGTGCA
AGCTGCTGCGCGGCGCCAAGGCCCTGACCGACATCGTGCCCTGACCGAGGAGGCCGAGCTG
GAGCTGGCCGAGAACCGCGAGATCCTGAAGGAGCCCGTGACGGCGTGTACTACGACCCAG
CAAGGACCTGATCGCCGAGATCCAGAAGCAGGGCAACGACCAAGTGACCTACCAGATCTACC
AGGAGCCCTTCAAGAACCTGCGCACCCGGCAAGTACGCCAAGATGCGCACCCGCCACACCAAC
GACGTGAAGCAGCTGGCCGAGGCCGTGCAGAAGATCACCCAGGAGAGCATCGTGATCTGGGG
CAAGACCCCCAAGTTCGCGCTGCCATCCCCAAGGAGACCTGGGAGACCTGGTGGAGCGACT
ACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTTTCGTGAACACCCCCCCCCCTGGTGAAGCTGT
GGTACCAGCTGGAGAAGGAGGCCATCGTGGGCGCCGAGACCTTCTACGTGGACGGCGCCGCC
AACCGCGAGACCAAGATCGGCAAGGCCGGCTACGTGACCGACAAGGGCCGCCAGAAGGTGG
TGAGCTTACCGAGACCACCAACCAGAAGACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAG
GACAGCGGCCCCGAGGTGAACATCGTGACCGACAGCCAGTACGCCCTGGGCATCATCCAGGC
CCAGCCCGACAAGAGCAGAGCGAGCTGGTGAGCCAGATCATCGAGCAGCTGATCAAGAAG
GAGAAGGTGTACCTGAGCTGGGTGCCCCGCCACAAGGGCATCGGCGGCAACGAGCAGGTGGA
CAAGCTGGTGAGCAGCGGCATCCGCAAGGTGCTGTTCTTGACGGCATCGACAAGGCCCAGG
AGGAGCACGAGAAGTACCACAGCAACTGGCGCGCCATGGCCAGCGAGTTCAACCTGCCCCC
ATCGTGGCCAAGGAGATCGTGGCCAGCTGCGACAAGTGCCAGCTGAAGGGCGAGGCCATGCA
CGGCCAGGTGGACTGCAGCCCCGGCATCTGGCAGCTGGACTGCACCCACCTGGAGGGCAAGA
TCATCCTGGTGGCCGTGCACGTGGCCAGCGGCTACATGGAGGCCGAGGTGATCCCCGCCGAG
ACCGGCCAGGAGACCGCTACTTCATCCTGAAGCTGGCCGGCCGCTGGCCCGTGAAGGTGATC
CACACCGACAACGGCAGCAACTTACCAGCACCGCCGTGAAGGCCGCCTGCTGGTGGGCCGA
CATCCAGCGGAGTTCCGCATCCCCTACAACCCCCAGAGCCAGGGCGTGGTGGAGAGCATGA
ACAAGGAGCTGAAGAAGATCATCGGCCAGGTGCGCGACCAGGCCGAGCACCTGAAGACCGCC
GTGCAGATGGCCGTGTTTCATCCACAACCTTCAAGCGCAAGGGCGGCATCGGCGGCTACAGCGC
CGGCGAGCGCATCATCGACATCATCGCCAGCGACATCCAGACCAAGGAGCTGCAGAAGCAGA
TCATCAAGATCCAGAACCTTCCGCGTGTACTACCGCGACAGCCGCGACCCCATCTGGAAGGGCC
CCGCCAAGCTGCTGTGGAAGGGCGAGGGCGCCGTGGTGATCCAGGACAACAGCGACATCAAG
GTGGTGCCCCGCCGCAAGGCCAAGATCATCAAGGACTACGGCAAGCAGATGGCCGGCGCCGA
CTGCGTGGCCGGCCGCCAGGACGAGGAC

FIGURE 74

Pol_TV2_C_ZAwt (SEQ ID NO:104)

TTTTTTAGGGAAAATTTGGCCTTCCCACAAGGGGAGGCCAGGGAATTCCTTCAGAGCAGACC
AGAGCCAAACAGCCCCACCACTAGAACCAACAGCCCCACCAGCAGAGAGCTTCAAGTTCAAGG
AGACTCCGAAGCAGGAGCCGAAAGACAGGGAACCTTTAACTTCCCTCAAATCACTCTTTGGCA
GCGACCCCTTGTCTCAATAAAAGTAGCGGGCCAAACAAAGGAGGCTCTTTTAGATACAGGAG
CAGATGATACAGTACTAGAAGAAATAAACTTGCCAGGAAAATGGAAACCAAAAAATGATAGG
AGGAATTGGAGGTTTTATCAAAGTAAGACAGTATGATCAAATACTTATAGAAAATTTGTGGAAA
AAGGGCTATAGGTACAGTATTAGTAGGACCTACACCTGTCAACATAATTGGAAGAAATCTGTT
GACTCAGCTTGGATGCACACTAAATTTTCCAATTAGCCCCATTGAAACTGTACCAGTAAAAAT
AAAGCCAGGAATGGATGGCCCAAAGGTTAAACAATGGCCATTGACAGAAGAAAAAATAAAA
GCATTAAACAGAAATTTGTGAGGAAATGGAGAAGGAAGGAAAAATTACAAAAATTGGGCCTGA
AAATCCATATAACACTCCAGTATTTGCCATAAAGAAGAAGGACAGTACAAAGTGGAGAAAAAT
TAGTAGATTTTCAGGGAACTCAATAAAGAAGAACTCAAGACTTTTGGGAAGTCCAATTAGGAATA
CCACACCCAGCAGGGTTAAAAAAGAAAAAATCAGTGACAGTACTGGATGTGGGAGATGCATA
TTTTTCAGTCCCTTTAGATGAGAGCTTCAGAAAAATATACTGCATTACCATACCTAGTATAAAC
AATGAAACACCAGGGATTAGATATCAATATAATGTTCTTCCACAGGGATGGAAAGGATCACC
AGCAATATTCCAGAGTAGCATGACAAGAATCTTAGAGCCCTTTAGAACACAAAAACCCAGAAAG
TAGTTATCTATCAATATATGGATGACTTATATGTAGGATCTGACTTAGAAATAGGGCAACATA
GAGCAAAAAATAGAGGAGTTAAGAGGACACCTATTGAAATGGGGATTTACCACACCAGACAAG
AAACATCAGAAAGAACCCCCATTTCTTTGGATGGGGTATGAACTCCATCCTGACAAATGGACA
GTACAGCCTATACAGCTGCCAGAAAAGGAGAGCTGGACTGTCAATGATATACAGAAGTTAGT
GGGAAAGTTAACTGGGCAAGTCAGATTTACCCAGGGATTAAAGTAAGGCAACTGTGTAAAC
TCCTTAGGGGAGCCAAAGCACTAACAGACATAGTGCCACTGACTGAAGAAGCAGAATTAGAA
TTGGCTGAGAACAGGGAAATTTCTAAAAGAACCAGTACATGGAGTATATTATGACCCATCAAA
AGATTTAATAGCTGAAATACAGAAACAGGGGAATGACCAATGGACATATCAAATTTACCAAG
AACCATTTAAAAATCTGAGAACAGGAAAGTATGCAAAAAATGAGGACTGCCACACTAATGAT
GTGAAACAGTTAGCAGAGGCAGTGCAAAAAGATAACCCAGGAAAGCATAGTAATATGGGGAA
AAACTCCTAAATTTAGACTACCCATCCCCAAAAGAAACATGGGAGACATGGTGGTCAGACTATT
GGCAAGCCACCTGGATTCCCTGAGTGGGAGTTTGTCATACCCCTCCCCTAGTAAAATTGTGGT
ACCAGCTGGAAAAAGAACCCATAGTAGGGGCAGAAAATTTCTATGTAGATGGAGCAGCCAAT
AGGGAAACTAAAAATAGGAAAAGCAGGGTATGTCACTGACAAAGGAAGGCAGAAAGTTGTTTC
CTTCACTGAAACAACAAATCAGAAAGCTGAATTACAAGCAATTCAGCTAGCTTTGCAGGATTC
AGGGCCAGAAGTAAACATAGTAACAGACTCACAGTATGCATTAGGAATCATTCAAGCACAAAC
CAGATAAGAGTGAATCAGAATTAGTCAGTCAAATAATAGAACAGTTGATAAAAAAGGAAAAA
GTCTACCTATCATGGGTACCAGCACATAAAGGAATTGGAGGAAATGAACAAGTAGACAAATT
AGTAAGTAGTGGAATCAGAAAAGTACTGTTTCTAGATGGAATAGATAAAGCTCAAGAAGAGC
ATGAAAAATATCACAGCAATTGGAGAGCAATGGCTAGTGAGTTAATCTGCCACCCATAGTA
GCAAAGGAAATAGTAGCCAGCTGTGATAAATGTCACTAAAAGGGGAAGCCATGCATGGACA
AGTCGACTGTAGTCCAGGAATATGGCAATTAGACTGTACACATTTAGAAGGAAAAATCATCCT
AGTAGCAGTCCATGTAGCCAGTGGCTACATGGAAGCAGAGGTTATCCCAGCAGAAACAGGAC
AAGAAACAGCATACTTTATACTAAAATTAGCAGGAAGATGGCCAGTCAAAGTAATACATACA
GATAATGGCAGTAATTTACCAGTACCGCAGTTAAGGCAGCCTGTTGGTGGGCAGATATCCAA
CGGAATTTGGAATTCCTACAATCCCCAAAGTCAAGGAGTAGTAGAATCCATGAATAAAGA
ATTAAAGAAAAATCATAGGGCAAGTAAGAGATCAAGCTGAGCACCTTAAGACAGCAGTACAAA
TGGCAGTATTCATTACAATTTTAAAAGAAAAAGGGGGGATTGGGGGTACAGTGCAGGGGAG
AGAATAATAGACATAATAGCATCAGACATACAAATAAAGAATTACAAAAACAAATTATAAA
AATTCAAAATTTTCGGGTTTATTACAGAGACAGCAGAGACCTATTTGGAAAGGACCAGCCAA
ACTACTCTGGAAGGTGAAGGGGCAGTAGTAATACAAGATAATAGTGATATAAAGGTAGTAC
CAAGAAGGAAAGCAAAAATCATTAAGGACTATGGAAAACAGATGGCAGGTGCTGATTGTGTG
GCAGGTAGACAGGATGAAGAT

FIGURE 75

Table 1. Demographic characteristics of the study population	
Age (years)	
Mean	65.2
SD	10.5
Range	45-85
Gender	
Male	58 (45.2%)
Female	67 (52.8%)
Ethnicity	
White	72 (56.8%)
Black	18 (14.2%)
Hispanic	12 (9.5%)
Other	18 (14.2%)
Education level	
High school or less	35 (27.8%)
Some college	28 (22.2%)
Bachelor's degree	22 (17.4%)
Master's degree	12 (9.5%)
PhD	8 (6.3%)
Marital status	
Married	65 (51.2%)
Divorced	15 (11.8%)
Widowed	22 (17.4%)
Single	10 (7.9%)
Employment status	
Employed	12 (9.5%)
Unemployed	53 (41.5%)
Retired	40 (31.5%)
Health insurance	
Medicare	68 (53.5%)
Medicaid	15 (11.8%)
Private	12 (9.5%)
Other	15 (11.8%)
Annual income	
<\$10,000	18 (14.2%)
\$10,000-\$20,000	22 (17.4%)
\$20,000-\$30,000	15 (11.8%)
>\$30,000	12 (9.5%)

FIGURE 76

FIGURE 76

RevExon1_TV2_C_ZAwt (SEQ ID NO:106)

ATGGCAGGAAGAAGCGGAGACAGCGACGAAGCGCTCCTCCAAGCAATAAAG
ATCATCAAGATCCTCTACCAAAGCA

FIGURE 77

FIGURE 77

RevExon2_TV2_C_ZAopt (SEQ ID NO:107)

CCCTACCCCAAGCCCGAGGGCACCCGCCAGGCCCGCCGCAACCGCCGCCGCC
GCTGGCGCGCCCGCCAGCAGCAGATCCACAGCATCAGCGAGCGCATCCTGGA
CACCTGCCTGGGCGCCCCACCAAGCCCGTGCCCTGCTGCTGCCCCCATCG
AGCGCCTGCACATCAACTGCAGCGAGAGCAGCGGCACCAGCGGCACCCAGT
AGAGCCAGGGCACCGCCGAGGGCGTGCGGCAACCCCTAA

FIGURE 78

FIGURE 78

RevExon2_TV2_C_ZAwt (SEQ ID NO:108)

ACCCTTATCCCAAACCCGAGGGGACCCGACAGGCTCGGAGGAATCGAAGAA
GAAGGTGGAGAGCAAGACAGCAGCAGATCCATTGATTAGTGAGCGGATTCT
TGACACTTGCCTGGGACGACCTACGAAGCCTGTGCCTCTTCTGCTACCACCGA
TTGAGAGACTTCATATTAATTGTAGTGAGAGCAGTGGAAGTTCTGGGACACA
GTAGTCTCAGGGGACTGCAGAGGGGGTGGGGAACCCTTAA

FIGURE 79

FIGURE 79

TatExon1_TV2_C_ZAopt (SEQ ID NO:109)

ATGGAGCCCATCGACCCCAACCTGGAGCCCTGGAACCACCCCGGCAGCCAGC
CCAAGACCGCCTGCAACGGCTGCTACTGCAAGCGCTGCAGCTACCACTGCCT
GGTGTGCTTCCAGAAGAAGGGCCTGGGCATCTACTACGGCCGCAAGAAGCGC
CGCCAGCGCCGCAGCGCCCCCCCCCAGCAACAAGGACCACCAGGACCCCCTGC
CCAAGCAG

FIGURE 80

FIGURE 80

TatExon1_TV2_C_ZAwt (SEQ ID NO:110)

ATGGAGCCAATAGATCCTAACCTAGAACCTGGAACCATCCAGGAAGTCAGC
CTAAAACTGCTTGTAATGGGTGTTACTGTAAACGTTGCAGCTATCATTGTCTA
GTTTGCTTTCAGAAAAAAGGCTTAGGCATTTACTATGGCAGGAAGAAGCGGA
GACAGCGACGAAGCGCTCCTCCAAGCAATAAAGATCATCAAGATCCTCTACC
AAAGCAG

FIGURE 81

FIGURE 81

TatExon2_TV2_C_ZAopt (SEQ ID NO:111)

CCCCTGAGCCAGACCCGCGGCGACCCACCGGCAGCGAGGAGAGCAAGAAG
AAGGTGGAGAGCAAGACCGCCGCCGACCCCTTCGACTAG

FIGURE 82

FIGURE 82

TatExon2_TV2_C_ZAwt (SEQ ID NO:112)

CCCTTATCCCAAACCCGAGGGGACCCGACAGGCTCGGAGGAATCGAAGAAG
AAGGTGGAGAGCAAGACAGCAGCAGATCCATTCGATTAG

FIGURE 83

FIGURE 83

Vif_TV2_C_ZAopt (SEQ ID NO:113)

ATGGAGAACCGCTGGCAGGTGCTGATCGTGTGGCAGGTGGACCGCATGAAGA
TCCGCACCTGGCACAGCCTGGTGAAGCACCACATGTACGTGAGCCGCCGCGC
CGACGGCTGGTTCTACCGCCACCACTACGAGAGCCGCCACCCCAAGGTGAGC
AGCGAGGTGCACATCCCCCTGGGCGACGCCC GCCTGGTGATCAAGACCTACT
GGGGCCTGCAGACCGGCGAGCGCGCCTGGCACCTGGGCCACGGCGTGAGCA
TCGAGTGGCGCCTGCGCCGCTACAGCACCCAGGTGGACCCCGACCTGACCGA
CCAGCTGATCCACATGCACTACTTCGACTGCTTCGCCGAGAGCGCCATCCGC -
AAGGCCATCCTGGGCCAGATCGTGAGCCCCAAGTGCGACTACCAGGCCGGCC
ACAACAAGGTGGGCAGCCTGCAGTACCTGGCCCTGACCGCCCTGATCAAGCC
CAAGAAGATCAAGCCCCCCTGCCAGCGTGCGCAAGCTGGTGGAGGACCGC
TGGAACAAGCCCCAGAAGACCCGCGGCCGCCGCGGCAACCACACCATGAAC
GGCCACTAG

FIGURE 84

105040-246660

Vif_TV2_C_ZAwt (SEQ ID NO:114)

ATGGAAAACAGATGGCAGGTGCTGATTGTGTGGCAGGTAGACAGGATGAAG
ATTAGAACATGGCACAGTTTAGTAAAGCACCATATGTATGTTTCGAGGAGAG
CTGATGGATGGTTCTACAGACATCATTATGAAAGCAGACACCCAAAAGTAAG
TTCAGAAGTACACATCCCATTAGGAGATGCCAGGTTAGTAATAAAAACATAT
TGGGGTCTGCAGACAGGAGAAAGAGCTTGGCATTGTTGGGTACGGAGTCTCCA
TAGAATGGAGATTGAGAAGATATAGCACACAAGTAGACCCTGACCTGACAG
ACCAACTAATTCATATGCATTATTTTGATTGTTTGCAGAATCTGCCATAAGG-
AAAGCCATACTAGGACAGATAGTTAGCCCTAAGTGTGACTATCAAGCAGGAC
ATAACAAGGTAGGATCTCTACAATACTTGGCACTGACAGCATTGATAAAACC
AAAAAAGATAAAGCCACCTCTGCCTAGTGTTAGGAAATTAGTAGAGGATAGA
TGGAACAAGCCCCAGAAGACCAGGGGCCGCAGAGGGAACCATAACAATGAAT
GGACACTAG

FIGURE 85

105040 3256660

Vpr_TV2_C_ZAopt (SEQ ID NO:115)

ATGGAGCAGGCCCCGAGGACCAGGGCCCCCAGCGCGAGCCCTACAACGAG
TGGACCCTGGAGCTGCTGGAGGAGCTGAAGCAGGAGGCCGTGCGCCACTTCC
CCCGCCCCCTGGCTGCACAACCTGGGCCCAGCACATCTACGAGACCTACGGCGA
CACCTGGACCGGCGTGGAGGCCATCATCCGCATCCTGCAGCAGCTGCTGTTC
ATCCACTTCCGCATCGGCTGCCACCACAGCCGCATCGGCATCCTGCGCCAGC
GCCGCGCCCGCAACGGCGCCAACCGCAGC

FIGURE 86

FIGURE 86

Vpr_TV2_C_ZAwt (SEQ ID NO:116)

ATGGAACAAGCCCCAGAAGACCAGGGGCCGCAGAGGGAACCATACAATGAA
TGGACACTAGAGCTTTTAGAAGAACTCAAGCAGGAAGCTGTCAGACACTTTC
CTAGACCATGGCTCCATAACTTAGGACAACATATCTATGAAACCTATGGAGA
TACTTGGACAGGAGTTGAAGCAATAATAAGAATCCTGCAACAATTACTGTTT
ATTCATTTTCAGGATTGGGTGCCATCATAGCAGAATAGGCATTTTGCGACAGA
GAAGAGCAAGAAATGGAGCCAATAGATCC

FIGURE 87

FIGURE 87

Vpu_TV2_C_ZAopt (SEQ ID NO:117)

ATGCTGGACCTGACCGCCCGCATCGACAGCCGCCTGGGCATCGGCGCCCTGA
TCGTGGCCCTGATCATCGCCATCATCGTGTGGACCATCGTGTACATCGAGTAC
CGCAAGCTGGTGCGCCAGCGCAAGATCGACTGGCTGGTGAAGCGCATCCGCG
AGCGCGCCGAGGACAGCGGCAACGAGAGCGAGGGCGACACCGAGGAGCTGA
GCACCCTGGTGGACATGGGGCACCTGCGCCTGCTGGACGCCAACGACGTGTA
A

FIGURE 88

FIGURE 88

Vpu_TV2_C_ZAwt (SEQ ID NO:118)

ATGTTAGATTTAAGTCAAGAATAGATTCTAGATTAGGAATAGGAGCATTGA
TAGTAGCACTAATCATAGCAATAATAGTGTGGACCATAGTATATATAGAATA
TAGGAAATTGGTAAGGCAAAGGAAAATAGACTGGTTAGTTAAAAGGATTAG
GGAAAGAGCAGAAGACAGTGGCAATGAGAGCGAGGGGGGATACTGAAGAATT
ATCGACACTGGTGGATATGGGGCATCTTAGGCTTTTGGATGCTAATGATGTGT
AA

FIGURE 89

gp120mod.TV1.delV2 (SEQ ID NO:119)

1 gaattcatgc gcgtgatggg caccagaag aactgccagc agtgggtggat ctggggcattc
61 ctgggcttct ggatgctgat gatctgcaac accgaggacc tgtgggtgac cgtgtactac
121 ggcgtgcccg tgtggcgcca cgccaagacc accctgttct gcgccagcga cgccaaggcc
181 tacgagaccg aggtgcacaa cgtgtgggcc acccagcct gcgtgcccac cgaccccaac
241 cccagggaga tcgtgtggg caacgtgacc gagaactca acatgtggaa gaacgacatg
301 gccgaccaga tgcacgagga cgtgatcagc ctgtgggacc agagcctgaa gccctgcgtg
361 aagctgaccc cctgtgcgt gaccctgaac tgcaccgaca ccaacgtgac cggcaaccgc
421 accgtgaccg gcaacagcac caacaacacc aacggcaccg gcatttaca catcgaggag
481 atgaagaact gcagcttcaa cgccggcgcc ggccgcctga tcaactgaa caccagcacc
541 atcaccagg cctgcccacaa ggtgagcttc gacccatcc ccatccacta ctgcgcccc
601 gccggctacg ccatcctgaa gtgcaacaac aagacctca acggcaccgg ccctgctac
661 aacgtgagca cgtgacgtg caccacggc atcaagcccg tggtagcac ccagctgctg
721 ctgaacggca gcctggcca ggaggggcatt atcatccga gcgagaacct gaccgagaac
781 accaagacca tcatgtgca cctgaacgag agcgtggaga tcaactgac cgccccaac
841 aacaacacc gcaagagcgt gcgcacggc ccggccagg cttctacgc caccaacgac
901 gtgatggca acatccgcca ggcccactgc aacatcagca ccgaccgctg gaacaagacc
961 ctgcagcagg tgatgaagaa gctgggcgag cacttccca acaagacat ccagttcaag
1021 cccacgccg gcggcgacct ggagatcacc atgcacagct tcaactgcc cggcgagttc
1081 ttctactgca acaccagca cctgttcaac agcacctacc acagcaaca cggcacctac
1141 aagtacaacg gcaacagcag cagccccatt accctgcagt gcaagatcaa gcagatcgtg
1201 cgcattgtgc agggcggtgg ccaggccacc tacgcccc ccacgcccg caacatcacc
1261 tgccgcagca acatcaccg catcctgctg acccgcgac gcggcttcaa caccaccaac
1321 aacaccgaga cttccgccc cgccggcggc gacatgcgcg acaactggcg cagcgagctg
1381 tacaagtaca aggtggtgga gatcaagccc ctgggcatcg ccccaacca ggccaagcgc
1441 cgcgtggtgc agcgcgagaa gcgctaactc gag

FIGURE 90

```

1  gaattcatgc gcgtgatggg caccagaag aactgccagc agtgggtggat ctgggggcac
61  ctgggcttct ggatgctgat gatctgcaac accgaggacc tgtgggtgac cgtgtactac
121 ggcgtgcccg tgtggcgcgga cgccaagacc accctgttct gcgccagcga cgccaaggcc
181 tacgagaccg aggtgcacaa cgtgtggggc acccacgcct gcgtgcccac cgaccccaac
241 cccagaggaga tcgtgctggg caacgtgacc gagaacttca acatgtggaa gaacgacatg
301 gccgaccaga tgcacgagga cgtgatcagc ctgtgggacc agagcctgaa gccctgctg
361 aagctgaccc ccctgtgctg gaccctgaac tgcaccgaca ccaacgtgac cggcaaccgc
421 accgtgaccg gcaacagcac caacaacacc aacggcaccg gcatctacaa catcgaggag
481 atgaagaact gcagcttcaa cgccggcgcc ggccgcctga tcaactgcaa caccagcacc
541 atcaccaggg cctgccccaa ggtgagcttc gaccccatcc ccattccacta ctgcgcccc
601 gccggctacg ccattcctgaa gtgcaacaac aagaccttca acggcaccgg cccctgctac
661 aacgtgagca ccgtgcagtg caccacggcg atcaagcccc tgggtgagcac ccagctgctg
721 ctgaacggca gcctggccga ggagggcac atcatccgca gcgagaacct gaccgagaac
781 accaagacca tcatcgtgca cctgaacgag agcgtggaga tcaactgcac ccgccccaac
841 aacaacaccc gcaagagcgt gcgcatcgcc cccggccagg ctttctacgc caccaacgac
901 gtgatcggca acatccgcca ggcccactgc aacatcagca ccgaccgctg gaacaagacc
961 ctgcagcagg tgatgaagaa gctgggcgag cacttcccc acaagaccat ccagttcaag
1021 cccacgccc gcggcgacct ggagatcacc atgcacagct tcaactgccg cggcgagttc
1081 ttctactgca acaccagcaa cctgttcaac agcacctacc acagcaacaa cggcacctac
1141 aagtacaacg gcaacagcag cagccccatc accctgcagt gcaagatcaa gcagatcgtg
1201 cgcattgtggc agggcggtgg ccaggccacc tacgcccccc ccattcgccg caacatcacc
1261 tgccgcagca acatcaccgg catcctgctg acccgcgacg gcggcttcaa caccaccaac
1321 aacaccgaga ctttcgccc cggcgggcgg gacatgcgcg acaactggcg cagcgagctg
1381 tacaagtaca aggtgggtgga gatcaagccc ctgggcatcg cccccacaa ggccaagcg
1441 cgcgtggtgc agcgcgagaa gcgcgccgtg ggcacggcg ccgtgttcct gggcttcctg
1501 ggcgcgccc gcagcaccat ggcgcgcccc agcatcacc tgaccgtgca ggcccgcag
1561 ctgctgagcg gcatcgtgca gcagcagagc aacctgctga aggccatcga ggcccagcag
1621 cacatgctgc agctgaccgt gtggggcatc aagcagctgc agggccgctg gctggccatc
1681 gagcgctacc tgaaggacca gcagctgctg ggcattctgg gctgcagcgg ccgcctgac
1741 tgcaccaccg ccgtgccttg gaacagcagc tggagcaaca agagcgagaa ggacatctgg
1801 gacaacatga cctggatgca gtgggaccgc gagatcagca actacaccgg cctgatctac
1861 aacctgctgg aggacagcca gaaccagcag gagaagaacg agaaggacct gctggagctg
1921 gacaagtgga acaacctgtg gaactggttc gacatcagca actggccctg gtacatctaa
1981 ctcgag

```

FIGURE 91

gp140mod.TV1.mut7.delV2 (SEQ ID NO:121)

1 gaattcatgc gcgtgatggg caccagaag aactgccagc agtggtggat ctggggcacc
61 ctgggcttct ggatgctgat gatctgaac accgaggacc tgtgggtgac cgtgtactac
121 ggcgtgcccg tgtggcgca cgccaagacc accctgttct gcgccagcga cgccaaggcc
181 tacgagaccg aggtgcacaa cgtgtgggcc acccagcct gcgtgcccac cgaccccaac
241 cccaggaga tcgtgctggg caactgacc gagaacttca acatgtggaa gaacgacatg
301 gccgaccaga tgcacgagga cgtgatcagc ctgtgggacc agagcctgaa gccctgcgtg
361 aagctgacc cctgtgctg gacctgaac tgcaccgaca ccaacgtgac cggcaaccgc
421 accgtgaccg gcaacagcac caacaacacc aacggcaccg gcacttaca catcgaggag
481 atgaagaact gcagcttcaa cgccggcgcc ggccgcctga tcaactgcaa caccagcacc
541 atcaccagg cctgccccaa ggtgagcttc gacccatcc ccatccacta ctgcgcccc
601 gccggtacg ccatcctgaa gtgcaacaac aagaccttca acggcaccgg cccctgctac
661 aacgtgagca ccgtgcagt caccacggc atcaagcccg tggtagcac ccagtctgtg
721 ctgaacggca gcctggccga ggaggcgacc atcatccgca gcgagaacct gaccgagaac
781 accaagacca tcatcgtgca cctgaacgag agcgtggaga tcaactgac cgccccaac
841 aacaacacc gcaagagcgt gcgcatcgcc cccggccagg ccttctacgc caccaacgac
901 gtgatcggca acatccgca ggccactgc aacatcagca ccgaccgtg gaacaagacc
961 ctgcagcagg tgatgaagaa gctggcgag cacttccca acaagaccat ccagtcaag
1021 cccacgccc gcggcgacct ggagatcacc atgcacagct tcaactccg cggcgagttc
1081 ttctactgca acaccagcaa cctgttcaac agcacctacc acagcaaaa cggcacctac
1141 aagtacaac gcaacagcag cagccccatc accctgcagt gcaagatcaa gcagatcgtg
1201 cgcatgtggc agggcgtggg ccaggccacc tacgcccc ccatcgccgg caacatcacc
1261 tgccgcagca acatcaccgg catctgctg acccgcgacg gcggcttcaa caccaccaac
1321 aacaccgaga cttccgccc cgccggcgcc gacatgcgcg acaactggcg cagcgagctg
1381 tacaagtaca agtggtgga gatcaagccc ctgggcatcg cccccacaa ggccatcagc
1441 agcgtggtgc agagcgagaa gagcgccgtg ggcatcgcg ccgtgttctt gggcttctg
1501 ggccgcccgc gcagaccat gggcgccgc agcatcacc tgaccgtgca ggccgcccag
1561 ctgctgagcg gcacgtgca gcagcagagc aacctgctga aggccatcga ggccagcag
1621 cacatgctgc agctgaccgt gtggggcacc aagcagctgc agggccgct gctggccatc
1681 gagcgtacc tgaaggacca gcagctgctg ggcatctggg gctgcagcgg ccgcctgac
1741 tgcaccaccg ccgtgccctg gaacagcagc tggagcaaca agagcgagaa ggacatctgg
1801 gacaacatga cctggatgca gtgggaccgc gagatcagca actacaccgg cctgatctac
1861 aacctgctgg aggacagca gaaccagcag gagaagaac agaaggacct gctggagctg
1921 gacaagtga acaacctgtg gaactggttc gacatcagca actggccctg gtacatctaa
1981 ctgag

FIGURE 92

gp160mod.TV1.delV1V2 (SEQ ID NO:122)

1 gaattcatgc gcgtgatggg caccagaag aactgccagc agtgggtggat ctggggcadc
61 ctgggcttct ggatgctgat gatctgcaac accgaggacc tgtgggtgac cgtgtactac
121 ggctgtcccc tgtggcgcga cgccaagacc accctgttct gcgccagcga cgccaaggcc
181 tacgagaccg aggtgcacaa cgtgtgggcc acccagcct gcgtgcccac cgaccccaac
241 cccagaggaga tctgtctggg caactgacc gagaacttca acatgtggaa gaacgacatg
301 gccgaccaga tgcacgagga cgtgatcagc ctgtgggacc agagcctgaa gccctgcgtg
361 aagctgacc cctgtgcgt gggcgccggc aactgcaaca ccagcaccat caccagggc
421 tgcccaagg tgagcttga cccatcccc atccactact gcgccccgc cggctacgcc
481 atcctgaagt gcaacaacaa gaccttcaac ggcaccggcc cctgtacaa cgtgagcacc
541 gtgcagtga cccacggcat caagcccgtg gtgagcacc agctgctgct gaacggcagc
601 ctggccgagg agggcatcat catcgcagc gagaacctga ccgagaacac caagaccatc
661 atcgtgcacc tgaacgagag cgtggagatc aactgcacc gccccaacaa caacaccgc
721 aagagcgtgc gcatcgcccc cggccaggcc ttctacgcca ccaacgacgt gatcggcaac
781 atccgccagg cccactgcaa catcagcacc gaccgtgga acaagacct gcagcagggt
841 atgaagaagc tggcgagca ctccccaa aagaccatcc agttcaagcc ccacgccggc
901 ggcgacctgg agatcccat gcacagctc aactgccgcg gcgagttct ctactgcaac
961 accagcaacc tgttaacag cacctaccac agcaacaac gcacctaaa gtacaacggc
1021 aacagcagca gcccacac cctgcagtgc aagatcaagc agatcgtgc catgtggcag
1081 ggctgtggcc agggcaccta cccccccc atcgccggca acatcacctg ccgcagcaac
1141 ataccggca tctgtgac ccgcgacggc ggcttcaaca ccaccaaaa caccgagacc
1201 ttccgcccc gcggcgccga catgcgcgac aactggcgca gcgagctgta caagtacaag
1261 gtggtggaga tcaagcccct gggcatcgcc cccaccaagg ccaagcgccg cgtggtgcag
1321 cgcgagaagc gcgccgtggg catcgccgcc gtgttctgg gtttctggg cgcgcggc
1381 agcaccatgg gcgccccag catcacctg accgtgcagg cccgccagct gctgagcggc
1441 atcgtgcagc agcagagcaa cctgtgaag gccatcgagg cccagcagca catgtgcag
1501 ctgacctgt ggggcatcaa gcagctgcag gcccgctgc tggccatga gcgtacctg
1561 aaggaccagc agctgctggg catctggggc tgcagcgcc gctgatctg caccaccgc
1621 gtgcctgga acagcagctg gagcaacaag agcgagaagg acatctggga caacatgacc
1681 tggatgcagt gggaccgca gatcagcaac tacaccggcc tgatctaaa cctgtggag
1741 gacagccaga accagcagga gaagaacgag aaggacctgc tggagctgga caagtggaac
1801 aacctgtgga actggttga catcagcaac tggccctggt acatcaagat ctcatcatg
1861 atcgtgggc gctgatcgg cctgcgcatc atctcgccg tgctgagcat cgtgaaccgc
1921 gtgcgccagg gctacagccc cctgagctc cagacctga cccagccc ccgcggcctg
1981 gaccgctgg gcggcatga ggaggaggc ggcgagcagg accgcgacc cagcatccgc
2041 ctggtgagc gtttctgag cctggcctgg gacgacctgc gcaacctgt cctgttcagc
2101 taccaccgc tgcgcgact catcctgat gccgtgcgcg ccgtggagct gctgggccac
2161 agcagcctgc gcggcctga gcgggctgg gagatcctga agtacctggg cagcctgggt
2221 cagtactgg gctggagct gaagaagag gccatcagc tctggacac catcgccatc
2281 accgtggccg agggcaccga ccgcatcatc gagctggtgc agcgcatctg ccgcgccatc
2341 ctgaacatcc cccgccgat ccgccaggc ttcgaggccg cctgtctga actcgag

FIGURE 93

gp160mod.TV1.delV2 (SEQ ID NO:123)

1 gaattcatgc gcgtgatggg caccagaag aactgccagc agtgggtggat ctggggcadc
61 ctgggcttct gtagtctgat gatctgaac accgaggacc tgtgggtgac cgtgtactac
121 ggctgtcccc tgtggcgcga cgccaagacc accctgttct gcgccagcga cgccaaggcc
181 tacgagaccg aggtgcacaa cgtgtgggcc acccacgcct gcgtgcccac cgaccccaac
241 cccagaggaga tcgtgctggg caactgacc gagaacttca acatgtggaa gaacgacatg
301 gccgaccaga tgcacgagga cgtgatcagc ctgtgggacc agagcctgaa gccctgcgtg
361 aagctgacc cctgtgcgt gacctgaac tgcaccgaca ccaactgac cggcaaccgc
421 accgtgaccg gcaacagcac caacaacacc aacggcaccg gcactacaa catcgaggag
481 atgaagaact gcagcttcaa cgccggcgcc ggccgcctga tcaactgcaa caccagcacc
541 atcaccagg cctgccccaa ggtgagcttc gacctatcc ccattcacta ctgcgcccc
601 gccggtacg ccactctgaa gtgcaacaac aagacctta acggcaccgg cccctgctac
661 aacgtgagca ccgtgcagt caccacggc atcaagccc tggtgagcac ccagctgctg
721 ctgaacggca gcctggccga ggagggcac atcatccga gcgagaacct gaccgagaac
781 accaagacca tcatctgca cctgaacgag agcgtggaga tcaactgcac cgccccaac
841 aacaacacc gcaagagcgt gcgcatcggc cccggccagg ccttctacgc caccaacgac
901 gtgatcggca acatccgca ggccactgc aacatcagca ccgaccgtg gaacaagacc
961 ctgcagcagg tgatgaagaa gctgggcgag cacttccca acaagaccat ccagttaag
1021 cccacgccg gcggcgacct ggagatcac atgcacagt tcaactgcc cggcgagttc
1081 ttacttgca acaccagcaa cctgttcaac agcacctacc acagcaaaa cggcacctac
1141 aagtacaac gcaacagcag cagccccatc accctgcagt gcaagatcaa gcagatcgtg
1201 cgcattgtgc agggcgtggg ccaggccacc tacgcccccc ccactgcgg caacatcac
1261 tgccgcagca acatcaccg catctgctg acccgcgacg gcggttcaa caccaccaac
1321 aacaccgaga ccttcgccc cgccggcgcc gacatgcgcg acaactggcg cagcgagctg
1381 tacaagtaca aggtgtgga gatcaagccc ctgggcatcg ccccaacca ggccaagcgc
1441 cgcgtgtgag agcgcgagaa gcgcgccgtg ggcatcggcg cctgttctt gggttctg
1501 ggccgcccg gcagcaccat ggccgccgc agcatcacc tgaccgtgca ggccgccag
1561 ctgctgagcg gcactgtgca gcagcagagc aacctgctga aggccatga ggccagcag
1621 cacatgctgc agctgaccgt gtggggcacc aagcagctgc agcccgctg gctggccatc
1681 gagcgtacc tgaaggacca gcagctgctg ggcatctggg gctgcagcgg ccgctgac
1741 tgcaccacc cgtgccctg gaacagcagc tggagcaaca agagcgagaa ggacatctg
1801 gacaacatga cctgatgca gtgggaccgc gagatcagca actacaccg cctgatctac
1861 aacctgctgg aggacagcca gaaccagcag gagaagaac agaaggacct gctggagctg
1921 gacaagtga acaacctgt gaactggtc gacatcagca actggcctg gtacatcaag
1981 atcttcatca tgatcgtgg cgccctgatc ggccgcgca tcatctgc cgtgctgagc
2041 atcgtgaacc gcgtgcgca gggtacagc cccctgagct tccagacct gacccacg
2101 cccgcggcc tggaccgct ggccggcatc gaggaggagg gcggcgagca ggaccgcgac
2161 cgcagcatcc gcctggtgag cggcttctg agcctggcct gggacgacct gcgcaacctg
2221 tgcctgttca gtaccaccg cctgcgcgac ttatctga tcgctgag cgccgtggag
2281 ctgctgggcc acagcagcct gcgcggcctg cagcgcgct gggagatcct gaagtacctg
2341 ggagcctgg tcagctactg ggccctggag ctgaagaaga gcgcatcag cctgctggac
2401 accatgcca taccgtggc cgagggcacc gaccgatca tcgagctgtg gcagcgcac
2461 tgccgcgca tctgaacat ccccgccgc atccgccagg gcttcgaggc cgccctgctg
2521 taactcgag

FIGURE 94

gp160mod.TV1.mut7.delV2 (SEQ ID NO:124)

1 gaattcatgc gcgtgatggg caccagaag aactgccagc agtggtggat ctggggcatc
 61 ctgggcttct g gatgctgat gatctgcaac accgaggacc tgtgggtgac cgtgtactac
 121 ggcggtcccc tgtggcgga cgccaagacc accctgttct gcgccagcga cgccaaggcc
 181 tacgagaccg aggtgcacaa cgtgtgggcc acccacgcct gcgtgcccac cgaccccaac
 241 cccagggaga tcgtgctggg caacgtgacc gagaacttca acatgtggaa gaacgacatg
 301 gccgaccaga tgcacgagga cgtgatcagc ctgtgggacc agagcctgaa gccctgcgtg
 361 aagctgacct ccctgtgcgt gacctgaac tgcaccgaca ccaacgtgac cggcaaccgc
 421 accgtgaccg gcaacagcac caacaacacc aacggcaccg gcacttaca catcgaggag
 481 atgaagaact gcagcttcaa cgccggcgcc ggccgctga tcaactgcaa caccagcacc
 541 atcaccagg cctgccccaa ggtgagcttc gacccatcc ccatccacta ctgcgcccc
 601 gccggctacg ccatcctgaa gtgcaacaac aagaccttca acggcaccgg ccctgctac
 661 aacgtgagca ccgtgcagtg caccacggc atcaagcccg tggtagcac ccagctgctg
 721 ctgaacggca gcctggccga ggagggcac atcatccgca gcgagaacct gaccgagaac
 781 accaagacca tcatcgtgca cctgaacgag agcgtggaga tcaactgcac cgccccaac
 841 aacaacacc gcaagagcgt gcgcatcggc ccggccagg cttctacgc caccaacgac
 901 gtgatcggca acatccgcca ggcccactgc aacatcagca ccgaccgctg gaacaagacc
 961 ctgcagcagg tgatgaagaa gctggcgag cacttccca acaagaccat ccagttcaag
 1021 cccacgcgg gcggcgacct ggagatcacc atgcacagct tcaactgcc cggcgagttc
 1081 ttctactgca acaccagcaa cctgttcaac agcacctacc acagcaacaa cggcacctac
 1141 aagtacaacg gcaacagcag cagccccatc accctgcagt gcaagatcaa gcagatcgtg
 1201 cgcattgtggc agggcggtgg ccaggccacc tacgcccccc ccatcgccgg caacatcacc
 1261 tgccgcagca acatcaccgg catctgctg acccgcgacg gcggcttcaa caccaccaac
 1321 aacaccgaga cttccgccc cgccggcggc gacatgcgag acaactggcg cagcgagctg
 1381 tacaagtaca aggtggtgga gatcaagccc ctgggcatcg ccccaacca ggccatcagc
 1441 agcgtgtgac agagcgagaa gagcgccgtg ggcatcggcg ccgtgttctt gggcttctg
 1501 ggccgcccgg gcagcaccat gggcgccgac agcatcacc tgaccgtgca ggcccggcag
 1561 ctgctgagcg gcactgtgca gcagcagagc aacctgctga aggccatcga ggcccagcag
 1621 cacatgctgc agctgaccgt gtggggcacc aagcagctgc agggccgct gctggccatc
 1681 gagcgctacc tgaaggacca gcagctgctg ggcatctggg gctgcagcgg ccgctgac
 1741 tgcaccaccg ccgtgccctg gaacagcagc tggagcaaca agagcgagaa ggacatctgg
 1801 gacaacatga cctggatgca gtgggaccgc gagatcagca actacaccgg cctgatctac
 1861 aacctgctgg aggacagcca gaaccagcag gagaagaac agaaggacct gctggagctg
 1921 gacaagtgga acaacctgtg gaactggttc gacatcagca actggccctg gtacatcaag
 1981 atcttcatca tgatcgtggg cgccctgac ggccctgcga tcatcttcgc cgtgctgagc
 2041 atcgtgaacc gcgtgcgcca gggctacagc cccctgagct tccagacct gacccccagc
 2101 ccccgccggc tggaccgctt gggcgccatc gaggaggagg gcggcgagca ggaccgcgac
 2161 cgcagcatcc gcctggtgag cggcttctg agcctggcct gggacgacct gcgcaacctg
 2221 tgcctgttca gctaccaccg cctgcgcgac tcatcctga tcgccgtgag cgcctggag
 2281 ctgctgggcc acagcagcct gcgcggcctg cagcgcggtt gggagatcct gaagtacctg
 2341 ggcagcctgg tgagctactg gggcctggag ctgaagaaga gcgccatcag cctgctggac
 2401 accatcgcca tcacctggc cgagggcacc gaccgcatca tcgagctggt gcagcgcatc
 2461 tgccgcgcca tctgaacat ccccgccgc atccgccagg gcttcgaggc cgccctgctg
 2521 taactcag

FIGURE 95

gp160mod.TV1.tpa1 (SEQ ID NO:125)

1 gtcgacgcca ccatggatgc aatgaagaga gggctctgct gtgtgctgct gctgtgtgga
 61 gcagtcttcg ttgcgccag cgccagcacc gaggacctgt gggtgaccgt gtactacggc
 121 gtgcccgtgt ggcgcgacgc caagaccacc ctgttctgcg ccagcgacgc caaggcctac
 181 gagaccgagg tgcacaacgt gtgggccacc cagcctgcg tgcccaccga cccaacccc
 241 caggagatcg tgctgggcaa cgtgaccgag aacttcaaca tgtggaagaa cgacatggcc
 301 gaccagatgc acgaggacgt gatcagcctg tgggaccaga gcctgaagcc ctgctgaag
 361 ctgaccccc tgtgctgac cctgaactgc accgacacca acgtgaccgg caaccgcacc
 421 gtgaccggca acagcaccaa caacaccaac ggcaccggca tctacaacat cgaggagatg
 481 aagaactgca gcttcaacgc caccaccgag ctgcgcgaca agaagcacia ggagtacgcc
 541 ctgttctacc gcctggacat cgtgcccctg aacgagaaca gcgacaacti cacctaccgc
 601 ctgatcaact gcaacaccag caccatcacc caggcctgcc ccaagtgtag ctgcacccc
 661 atccccatcc actactgcgc cccgcgcggc tacgcatcc tgaagtgcaa caacaagacc
 721 ttcaacggca cgggccctg ctacaacgtg agcaccgtgc agtgacacca cggcatcaag
 781 cccgtggtga gcaccagct gctgctgaac ggcagcctgg ccgaggaggg catcatcatc
 841 cgcagcgaga acctgaccga gaacaccaag accatcatcg tgcacctgaa cgagagcgtg
 901 gagatcaact gcaccgccc caacaacaac acccgcaaga gcgtgcgcat cggccccggc
 961 caggccttct acgccacaa cgacgtgatc ggcaacatcc gccaggccca ctgcaacatc
 1021 agcaccgacc gctggaacaa gacctgcag cagggtgatga agaagctggg cgagcacttc
 1081 cccaacaaga ccatccagtt caagccccac gccggcggcg acctggagat caccatgcac
 1141 agcttcaact gccgcggcga gttctctac tgcaacacca gcaacctgtt caacagcacc
 1201 taccacagca acaacggcac ctacaagtac aacggcaaca gcagcagccc catcacctg
 1261 cagtgaaga tcaagcagat cgtgcgcatg tggcagggcg tgggccaggc cacctacgcc
 1321 ccccccatcg ccggcaacat cacttgccgc agcaacatca ccggcatcct gctgaccgc
 1381 gacggcggct tcaacaccac caacaacacc gagaccttc gccccggcgg cgcgacatg
 1441 cgcgacaact ggcgacgca gctgtacaag tacaaggtgg tgagatcaa gccctgggc
 1501 atgccccca ccaaggccaa gcgccgctg gtgcagcgcg agaagcgcg cgtgggcatc
 1561 ggcgccgtgt tctggggtt cctgggcgc gccggcagca ccatgggcgc cgccagcatc
 1621 acctgaccg tcaggcccc ccagctgctg agcggcatcg tgcagcagca gagcaacctg
 1681 ctgaaggcca tcaggccca gcagcacatg ctgcagctga ccgtgtgggg catcaagcag
 1741 ctgcaggccc gcgtgctggc catcagcgc tacctgaagg accagcagct gctgggcatc
 1801 tggggctgca gcggccgct gatctgcacc accgccgtgc cctggaacag cagctggagc
 1861 aacaagagcg agaaggacat ctgggacaac atgacctgga tgcagtggga ccgcgagatc
 1921 agcaactaca ccggcctgat ctacaacctg ctggaggaca gccagaacca gcaggagaag
 1981 aacgagaagg acctgctgga gctggacaag tggaacaacc tgtggaactg gtgcacatc
 2041 agcaactggc cctggtacat caagatcttc atcatgatcg tggcggcct gatcggcctg
 2101 cgcatcatct tcgcccgtgt gagcatcgtg aaccgcgtgc gccagggcta cagccccctg
 2161 agcttcaga cctgacccc cagccccgc gccctggacc gcctgggcgg catcaggagg
 2221 gagggcggcg agcaggaccg cgaccgcagc atccgcctgg tgagcggctt cctgagcctg
 2281 gcctgggacg acctgcgcaa cctgtgcctg ttacgtacc accgcctgcg cgacttcac
 2341 ctgatcgccg tgcgcgccgt ggagctgctg ggccacagca gcctgcgcgg cctgcagcgc
 2401 ggctgggaga tctgaagta cctgggcagc ctggtgcagt actggggcct ggagctgaag
 2461 aagagcgcca tcagcctgct ggacaccatc gccatcaccg tggccgaggg caccgaccgc
 2521 atcatcgagc tgggtgcagc catctgccgc gccatcctga acatccccg ccgcatccgc
 2581 cagggttcg aggcgcctt gctgtaactc gag

FIGURE 96

1 gaattcatgc gcgtgatggg caccagaag aactgccagc agtgggtgat ctggggcatc
 61 ctgggcttct ggatgctgat gatctgcaac accgaggacc tgtgggtgac cgtgtactac
 121 ggctgccccg tgtggcgga cgcaagacc accctgttct gcgccagcga cgcaaggcc
 181 tacgagaccg aggtgcacaa cgtgtgggcc acccagcct gcgtgccac cgacccaac
 241 cccaggaga tcgtgtggg caacgtgacc gagaacttca acatgtggaa gaacgacatg
 301 gccgaccaga tgcacgagga cgtgatcagc ctgtgggacc agagcctgaa gccctgcgtg
 361 aagctgacct cctgtgctg gacctgaac tgcaccgaca ccaacgtgac cggcaaccgc
 421 accgtgaccg gcaacagcac caacaacacc aacggcaccg gcatctacaa catcgaggag
 481 atgaagaact gcagcttcaa cgccaccacc gagctgcgcg acaagaagca caaggagtac
 541 gccctgttct accgcctgga catcgtgccc ctgaacgaga acagcgacaa cttcacctac
 601 cgctgatca actgcaacac cagcaccatc acccaggcct gcccgaagt gagcttcgac
 661 cccatcccca tccactactg cgccccgcc ggctacgcca tctgaagtg caacaacaag
 721 acctcaacg gcaccggccc ctgtacaac gtgagcaccg tgcagtgcac ccacggcatc
 781 aagcccgctg tgagcaccga gctgctgtg aacggcagcc tggccgagga gggcatcatc
 841 atccgcagcg agaacctgac cgagaacacc aagaccatca tcgtgcacct gaacgagagc
 901 gtggagatca actgcacccg cccaacaac aacaccgcga agagcgtgcg catcggcccc
 961 ggccaggcct tctagccac caacgacgtg atcggaaca tccgccaggc cactgcaac
 1021 atcagcaccg accgctggaa caagacctg cagcaggatga tgaagaagct gggcgagcac
 1081 tccccaaac agaccatcca gttcaagccc cagccggcg gcgacctgga gatcaccatg
 1141 cacagcttca actgccgagg cgagtcttc tactgcaaca ccagcaacct gttcaacagc
 1201 acctaccaca gcaacaacgg cacctacaag tacaacggca acagcagcag ccccatcacc
 1261 ctgcagtgca agatcaagca gatcgtgcgc atgtggcagg gcgtgggcca ggccacctac
 1321 gccccccca tcgccggcaa catcacctgc cgcagcaaca tcaccggcat cctgctgacc
 1381 cgcgacggcg gttcaacac caccaacaac accgagacct tccgccccgg cggcggcgac
 1441 atgcgcgaca actggcgagc cgagctgtac aagtacaagg tgggtggagat caagccccctg
 1501 ggcacgccc ccaccaaggc caagcgccgc gtgtgagcgc gcgagaagcg cgccgtgggc
 1561 atcgcgccg tgttctggg ctctctgggc gccgccggca gcaccatggg cgccgccagc
 1621 atcacctga ccgtgcagcg ccgccagctg ctgagcgga tcgtgcagca gcagagcaac
 1681 ctgtgaagg ccatcgaggc ccagcagcac atgtgcagc tgaccgtgtg gggcatcaag
 1741 cagctgcagg ccgcgtgct ggccatcgag cgctacctga aggaccagca gctgctgggc
 1801 atctggggct gcagcgccg cctgatctgc accaccgccg tgcctggaa cagcagctgg
 1861 agcaacaaga gcgagaagga catctgggac aacatgacct ggatgcagtg ggaccgcgag
 1921 atcagcaact acaccggcct gatctacaac ctgctggagg acagccagaa ccagcaggag
 1981 aagaacgaga aggacctgct ggagctggac aagtgaaca acctgtggaa ctggttcgac
 2041 atcagcaact ggccctggta catcaagatc tcatcatga tcgtgggagg cctgatcggc
 2101 ctgcgatca tcttcgccg gctgagcatc gtgaaccgcg tgcgccaggg ctacagcccc
 2161 ctgagcttcc agacctgac cccagcccc cgcggcctgg accgcctggg cggcatcgag
 2221 gaggagggcg gcgagcagga ccgcgaccgc agcatccgc tggtagcgg ctctctgagc
 2281 ctggcctggg acgacctgcg caacctgtgc ctgttcagct accaccgcct gcgcgacttc
 2341 atcctgatcg ccgtgcgcgc cgtggagctg ctgggccaca gcagcctgcg cggcctgcag
 2401 cgcggctggg agatcctgaa gtacctgggc agcctggtgc agtactggg cctggagctg
 2461 aagaagagcg ccatcagcct gctggacacc atgccatca ccgtggccga gggcaccgac
 2521 cgcatcatcg agctggtgca gcgcatctgc cgcgccatcc tgaacatccc ccgccgcatc
 2581 cgccagggct tcgaggccgc cctgctgtaa ctcgag

FIGURE 97

1 gaattcatga gagtgatggg gacacagaag aattgtcaac aatggtggat atggggcatc
 61 ttaggcttct ggatgctaata gatttgaac accgaggacc tgtgggtgac cgtgtactac
 121 ggcggtgccc tgtggcgca cgccaagacc accctgttct gcgccagcga cgccaaggcc
 181 tacgagaccg aggtgcacaa cgtgtgggcc acccagcct gcgtgcccac cgacccaac
 241 cccaggaga tcgtgtggg caacgtgacc gagaactca acatgtggaa gaacgacatg
 301 gccgaccaga tgcacgagga cgtgatcagc ctgtgggacc agagcctgaa gccctgcgtg
 361 aagctgacct ccctgtgctg gacctgaac tgcaccgaca ccaacgtgac cggcaaccgc
 421 accgtgaccg gcaacagcac caacaacacc aacggcaccg gcatctacaa catcaggag
 481 atgaagaact gcagcttcaa cgccaccacc gagctgcgcg acaagaagca caaggagtac
 541 gccctgttct accgctgga catcgtgcc ctgaacgaga acagcgacaa ctacacac
 601 cgctgatca actgcaacac cagcaccatc acccaggcct gccccagggt gagcttcgac
 661 cccatcccca tccactactg cgcctccgcc ggctacgcca tctgaagtg caacaacaag
 721 accttcaacg gcaccggccc ctgctacaac gtgagcaccg tgcagtgcac ccacggcatc
 781 aagcccgctg tgagcaccca gctgctgctg aacggcagcc tggccgagga gggcatcatc
 841 atccgcagcg agaacctgac cgagaacacc aagaccatca tcgtgcacct gaacgagagc
 901 gtggagatca actgacccc cccaacaac aacaccgcga agagcgtgcg catcgcccc
 961 ggccaggcct tctacgccac caacgacgtg atcggcaaca tccgccagge ccaactgcaac
 1021 atcagcaccg accgctggaa caagacctg cagcagggtga tgaagaagct gggcgagcac
 1081 tccccaaaca agaccatcca gttcaagccc cagccggcg gcgacctgga gatcacatg
 1141 cacagcttca actgccggcg cgagttctt tactgcaaca ccagcaacct gttcaacagc
 1201 acctaccaca gcaacaacgg cacctacaag tacaacggca acagcagcag ccccatcacc
 1261 ctgcagtga agatcaagca gatcgtgcgc atgtggcagg gcgtgggcca ggccacctac
 1321 gccccccca tcgccggcaa catcacctgc cgcagcaaca tcaccggcat cctgtgacc
 1381 cgcgacggcg gttcaaacac caccaacaac accgagacct tccgccccgg cggcggcgac
 1441 atgcgcgaca actggcgag cgagctgtac aagtacaagg tggtaggat caagccctg
 1501 ggcacgccc ccaccaaggc caagcgccgc gtgtgagcgc gcgagaagcg cgccgtgggc
 1561 atcggcgcg tgttctggg ctctctggg gccgcccga gcacatggg cgccgccagc
 1621 atcacctga ccgtgcaggc ccgccagctg ctgagcggca tcgtgcagca gcagagcaac
 1681 ctgtgaagg ccatcgaggc ccagcagcac atgtgcagc tgacctgtg gggcatcaag
 1741 cagctgcagg cccgctgct ggccatcgag cgtacctga aggaccagca gctgtgggc
 1801 atctggggct gcagcgccg cctgatctgc accaccgccc tgccttgaa cagcagctg
 1861 agcaacaaga gcgagaagga catctgggac aacatgacct ggatgcagtg ggaccgcgag
 1921 atcagcaact acaccggcct gatctacaac ctgctggagg acagccagaa ccagcaggag
 1981 aagaacgaga aggacctgct ggagctggac aagtgaaca acctgtgaa ctggttcgac
 2041 atcagcaact ggccctgga catcaagatc tcatcatga tcgtgggagg cctgatcgcc
 2101 ctgcgcatca tcttcgccgt gctgagcatc gtgaaccgcg tgcgccaggg ctacagcccc
 2161 ctgagcttcc agacctgac cccagcccc cgcggcctgg accgctggg cggcacgag
 2221 gaggagggcg gcgagcagga ccgcgaccgc agcatccgcc tggtagcgg ctctctgagc
 2281 ctggcctggg acgacctgc caacctgtgc ctgttcagct accaccgct gcgcgacttc
 2341 atcctgatcg ccgtgcgcgc cgtggagctg ctgggccaca gcacctgcg cggcctgcag
 2401 cgcggctggg agatctgaa gtacctgggc agcctggtgc agtactggg cctggagctg
 2461 aagaagagcg ccatcagcct gctggacacc atcgccatca ccgtggccga gggcaccgac
 2521 cgcatcatcg agctggtgca gcgcatctgc cgcgccatcc tgaacatccc ccgcccac
 2581 cgccagggtc tcgaggccgc cctgctgaa ctgag

FIGURE 98

Wild-type Env gp160 (8_2_ZA) (SEQ ID NO:128)

1 atgagagtga tggggacaca gaagaattgt caacaatggt ggatatgggg catcttaggc
61 ttctggatgc taatgatttg taacacggag gacttgtggg tcacagtcta ctatggggta
121 cctgtgtgga gagacgcaaa aactactcta ttctgtgcat cagatgctaa agcatatgag
181 acagaagtgc ataattgtctg ggctacacat gcctgtgtac ccacagaccc caaccacaa
241 gaaatagttt tgggaaatgt aacagaaaat ttaatatgt ggaaaaatga catggcagat
301 cagatgcatg aggatgtaat cagtttatgg gatcaaagcc taaagccatg tgtaaagttg
361 acccactct gtgtcacttt aaactgtaca gatacaaatg ttacaggtaa tagaactgtt
421 acaggtataa gtaccaataa tacaatggt acaggtatgt ataacttga agaaatgaaa
481 aattgctctt tcaatgcaac cacagaatta agagataaga aacataaaga gtatgcactc
541 tttatagac ttgatatagt accacttaat gagaatagt acaactttac atatagatta
601 ataaattgca atacctcaac cataacacaa gcctgtccaa aggtctcttt tgaccgatt
661 cctatacatt actgtgtccc agctggttat gcgattctaa agtgaataa taagacattc
721 aatgggacag gaccatgta taatgtcagc acagtacaat gtacacatgg aattaagcca
781 gtggtatcaa ctcaattact gttaaatggt agtctagcag aagaagggat aataattaga
841 tctgaaaatt tgacagagaa taccaaaaca ataatgtac acctaatga atctgtagag
901 attaattgta caagaccaa caataataca agaaaaagt taaggatagg accaggacaa
961 gcattctatg caacaaatga tgtaatagga aacataagac aagcacattg taacattagt
1021 acagatagat ggaacaaaac tttaacacag gtaatgaaaa aattaggaga gcatttcct
1081 aataaaacaa tacaatttaa accacatgca ggaggggatc tagaaattac aatgcatagc
1141 ttaattgta gaggagaatt ttctattgt aatacatcaa acctgtttaa tagcacatac
1201 cactctaata atggtacata caaatacaat ggtaattcaa gctcaccat cacactcaa
1261 tgtaaaataa aacaaattgt acgcatgtgg caaggggtag gacaagcaac gtatgcccc
1321 cccattgcag gaaacataac atgtgatca aacatcacag gaatactatt gacacgtgat
1381 ggaggattta acaccacaaa caacacagag acattcagac ctggaggagg agatatgagg
1441 gataactgga gaagtgaatt atataaatat aaagtagtag aaattaagcc attgggaata
1501 gcaccacta aggcaaaaag aagagtgtg cagagagaaa aaagagcagt gggaatagga
1561 gctgtgttcc ttgggttctt gggagcagca ggaagcacta tgggcgcagc gtcaataacg
1621 ctgacggtac aggccagaca actgtgtctt ggtatagtgc aacagcaaag caatttgcgt
1681 aaggctatag aggcgcaaca gcatatgtt caactcacag tctggggcat taagcagctc
1741 caggcgagag tcctggctat agaaagatac ctaaaggatc aacagctcct agggatttgg
1801 ggctgctctg gaagactcat ctgcaccact gctgtgcctt ggaactccag ttggagtaat
1861 aaatctgaaa aagatatatt ggataacatg acttggatgc agtgggatag agaaattagt
1921 aattacacag gcttaataa caatttgcct gaagactcgc aaaaccagca ggaaaagaat
1981 gaaaaagatt tattagaatt ggacaagtgg aacaatctgt ggaattggtt tgacatatca
2041 aactggccgt ggtatataaa aatattcata atgatagtag gaggcttgat aggtttaaga
2101 ataattttg ctgtgcttct tatagtgaat agagttaggc agggatactc acctttgtca
2161 ttcagaccc ttacccaag cccgagggga ctcgacaggc tcggaggaat cgaagaagaa
2221 ggtggagagc aagacagaga cagatccata cgatttgtga gcgattctt gtcgcttgc
2281 tgggacgatc tgcggaacct gtgcctcttc agctaccacc gcttgagaga ctcatatta
2341 attgcagtga gggcagtgga acttctggga cacagcagtc tcaggggact acagaggggg
2401 tgggaaatcc ttaagtatct gggaagtctt gtgcaatatt ggggtctaga gtaaaaaag
2461 agtgctatta gtctgcttga taccatagca ataacagtag ctgaaggaac agataggatt
2521 atagaattag tacaagaat ttgtagagct atcctcaaca tacctagaag aataagacag
2581 ggctttgaag cagctttgct ataa

FIGURE 99

gp140mod.TV1.tpa1 (SEQ ID NO:131)

1 atggatgcaa tgaagagagg gctctgctgt gtgctgctgc tgtgtggagc agtcttcgtt
61 tcgcccagcg ccagcaccga ggacctgtgg gtgaccgtgt actacggcgt gcccggtgg
121 cgcgacgcca agaccacct gtctgcgcc agcgacgcca aggcctacga gaccgaggtg
181 cacaacgtgt gggccacca cgcctgcgtg cccaccgacc ccaaccccca ggagatcgtg
241 ctgggcaacg tgaccgagaa cttcaacatg tggaagaacg acatggccga ccagatgcac
301 gaggacgtga tcagcctgtg ggaccagagc ctgaagccct gcgtgaagct gacccccctg
361 tgcgtgacct tgaactgcac cgacaccaac gtgaccggca accgcaccgt gaccggcaac
421 agcaccaaca acaccaacgg caccggcatc tacaacatcg aggagatgaa gaactgcagc
481 ttcaacgcca ccaccgagct gcgcgacaag aagcacaagg agtacgccct gttctaccgc
541 ctggacatcg tgccctgaa cgagaacagc gacaacttca cctaccgcct gatcaactgc
601 aacaccagca ccatcacca ggctgcccc aaggtgagct tcgaccccat ccccatccac
661 tactgcgcc cgcgggcta cgccatcctg aagtgaaca acaagacctt caacggcacc
721 ggccccctgt acaacgtgag caccgtgcag tgacccacg gcatcaagcc cgtggtgagc
781 acccagctgc tgctgaacgg cagcctggcc gaggagggca tcatcatccg cagcgagaac
841 ctgaccgaga acaccaagac catcatcgtg cacctgaacg agagcgtgga gatcaactgc
901 acccgcccca acaacaacac cgcgaagagc gtgcgcatcg gccccggcca ggcttctac
961 gccaccaacg acgtgatcgg caacatccgc caggccact gcaacatcag caccgaccgc
1021 tggaacaaga cctgcagca ggtgatgaag aagctgggcg agcacttccc caacaagacc
1081 atccagtcca agccccacgc cggcggcgac ctggagatca ccatgcacag cttcaactgc
1141 cgcggcgagt tcttctactg caacaccagc aacctgttca acagcaccta ccacagcaac
1201 aacggcacct acaagtataa cggcaacagc agcagcccca tcacctgca gtgcaagatc
1261 aagcagatcg tgcgcatgtg gcagggcgtg ggccaggcca cctacgcccc cccatcgcc
1321 ggcaacatca cctgccgcag caacatcacc ggcatcctgc tgacccgga cggcggttc
1381 aacaccacca acaacaccga gacctccgc cccggcggcg gcgacatcg cgacaactgg
1441 cgcagcgagc tgtacaagta caaggtggtg gagatcaagc cctggggcat cgccccacc
1501 aaggccaagc gccgcgtggt gcagcgcgag aagcgcgccg tgggcatcgg cgccgtgttc
1561 ctgggcttcc tgggcgccgc cggcagcacc atgggcgccg ccagcatcac cctgaccgtg
1621 caggccccgc agctgctgag cggcatcgtg cagcagcaga gcaacctgct gaaggccatc
1681 gaggccccagc agcatatgct gcagctgacc gtgtggggca tcaagcagct gcaggccccgc
1741 gtgctggcca tcgagcgcta cctgaaggac cagcagctgc tgggcatcgt gggtgcagc
1801 ggccgcctga tctgcaccac cgccgtgccc tggaacagca gctggagcaa caagagcgag
1861 aaggacatct gggacaacat gacctggtg cagtgggacc gcgagatcag caactacacc
1921 ggctgatct acaacctgct ggaggacagc cagaaccagc aggagaagaa cgagaaggac
1981 ctgctggagc tggacaagtg gaacaacctg tggaactggt tcgacatcag caactggccc
2041 tggatcatct aa

FIGURE 100

gp140mod.TV1 (SEQ ID NO:132)

1 gaattcatgc gctgatggg caccagaag aactgccagc agtgggtgat ctggggcatc
 61 ctgggcttct ggatgctgat gatctgcaac accgaggacc tgtgggtgac cgtgtactac
 121 ggcggtcccc gtgtggcgca cgccaagacc accctgttct gcgccagcga cgccaaggcc
 181 tacgagaccg aggtgcacaa cgtgtgggcc acccagcct gcgtgccac cgacccaac
 241 cccaggaga tcgtgctggg caacgtgacc gagaactca acatgtggaa gaacgacatg
 301 gccgaccaga tgcagagga cgtgatcagc ctgtgggacc agagcctgaa gccctgcgtg
 361 aagctgaccc cctgtgctg gacctgaac tgcaccgaca ccaacgtgac cggcaaccgc
 421 accgtgaccg gcaacagcac caacaacacc aacggcaccg gcatctacaa catcgaggag
 481 atgaagaact gcagcttcaa cgccaccacc gagctgcgcg acaagaagca caaggagtac
 541 gccctgttct accgctgga catcgtcccc ctgaacgaga acagcgacaa ctacacctac
 601 cgcctgatca actgcaacac cagcaccatc acccaggcct gcccgaagg gagcttcgac
 661 cccatcccca tccactactg cgccccgcc ggctacgcca tctgaagt caacaacaag
 721 acctcaacg gcaccggccc ctgtacaaac gtgagcaccg tgcagtgcac ccacggcatc
 781 aagcccgtgg tgcacccca gctgctgctg aacggcagcc tggccgagga gggcatcatc
 841 atcgcagcg agaacctgac cgagaacacc aagaccatca tcgtgcacct gaacgagagc
 901 gtggagatca actgcaccg cccaacaac aacaccgca agagcgtgcg catcgcccc
 961 ggccaggcct tctacgccac caacgacgtg atcggaaca tccgccaggc ccactgcaac
 1021 atcagcaccg accgtggaa caagaccctg cagcaggtga tgaagaagct gggcgagcac
 1081 tccccaaaca agaccatcca gttaagccc cagccggcg gcgacctgga gatcaccatg
 1141 cacagttca actgccgcg cgagttctt tactgaaca ccagcaacct gttaacagc
 1201 acctaccaca gcaacaacg cacctacaag tacaacggca acagcagcag cccatcacc
 1261 ctgcagtgca agatcaagca gatcgtgcgc atgtggcagg gcgtgggcca ggccacctac
 1321 gccccccca tcgccggcaa catcacctgc cgcagcaaca tcaccggcat cctgtgacc
 1381 cgcgacggcg gttcaacac caccaacaac accgagacct tccgcccgg cggcggcgac
 1441 atcgcgcaca actggcgag cgagctgtac aagtacaagg tgggtggagat caagcccctg
 1501 ggcatcgccc ccaccaaggc caagcggcg gtggtgcagc gcgagaagcg cgccgtgggc
 1561 atcggcggcg tgttctggg ctctctggg gccgcccga gcacctggg cgccggcagc
 1621 atcacctga cgtgcaggc ccgcagctg ctgagcggca tcgtgcagca gcagagcaac
 1681 ctgtgaagg ccatcgagg ccagcagcac atgtgcagc tgaccgtgtg gggcatcaag
 1741 cagctgcagg cccgcgtgct ggcatcgag cgctacctga aggaccagca gctgctgggc
 1801 atctggggct gcagcggcg cctgatctgc accaccgccc tgcctggaa cagcagctgg
 1861 agcaacaaga gcgagaagga catctgggac aacatgacct ggatgcagtg ggaccgcgag
 1921 atcagcaact acaccggcct gatctacaac ctgctggagg acagccagaa ccagcaggag
 1981 aagaacgaga aggacctgct ggagctggac aagtgaaca acctgtggaa ctggttcgac
 2041 atcagcaact ggccctggta catctaactc gag

FIGURE 101

gp140mod.TV1.wtLnative (SEQ ID NO:133)

1 gaattcatga gagtgatggg gacacagaag aattgtcaac aatggtggat atggggcatc
61 ttaggtcttct ggatgctaata gatttgaac accgaggacc tgtgggtgac cgtgtactac
121 ggcggtgccc tgtggcgcca cgccaagacc accctgttct gcgccagcga cgccaaggcc
181 tacgagaccg aggtgcacaa cgtgtgggcc acccagcct gcgtgcccac cgacccaac
241 ccccaggaga tcgtgctggg caacgtgacc gagaacttca acatgtggaa gaacgacatg
301 gccgaccaga tgcacgagga cgtgatcagc ctgtgggacc agagcctgaa gccctgcgtg
361 aagctgacc cctgtgcgt gacctgaac tgcaccgaca ccaacgtgac cggcaaccgc
421 accgtgaccg gcaacagcac caacaacacc aacggcaccg gcactacaa catcgaggag
481 atgaagaact gcagcttcaa cgccaccacc gagctgcgcg acaagaagca caaggagtag
541 gccctgttct accgcttga catcgtgccc ctgaacgaga acagcgacaa cttcacctac
601 cgcctgatca actgcaacac cagcaccatc acccaggcct gcccgaaggt gagttcgac
661 cccatcccca tccactactg cgccccgcc ggctacgcca tctgaagtg caacaacaag
721 accttcaacg gcaccggccc ctgtacaac gtgagcaccg tgcagtgcac ccacggcatc
781 aagcccgtgg tgagcaccca gctgctgctg aacggcagcc tggccgagga gggcatcatc
841 atccgcagcg agaacctgac cgagaacacc aagaccatca tcgtgcacct gaacgagagc
901 gtggagatca actgcaccg cccaacaac aacaccgcga agagcgtgcg catcgccccc
961 ggccaggcct tctagccac caacgacgtg atcggcaaca tccgccaggc cactgcaac
1021 atcagcaccg accgctggaa caagacctg cagcaggtga tgaagaagct gggcgagcac
1081 tcccccaaca agaccatcca gttcaagccc cagccggcg gcgacctgga gatcaccatg
1141 cacagttca actgccgcg cgagttctt tactgcaaca ccagcaacct gttcaacagc
1201 acctaccaca gcaacaacgg cacctacaag tacaacggca acagcagcag cccatcac
1261 ctgcagtgca agatcaagca gatcgtgcgc atgtggcagg gcgtgggcca ggccacctac
1321 gccccccca tcgccggcaa catcacctgc cgcagcaaca tcaccggcat cctgctgacc
1381 cgcgacggcg gttcaacac caccaacaac accgagacct tccgccccgg cggcgcgac
1441 atgcgcgaca actggcgag cgagctgtac aagtacaagg tggaggagat caagcccctg
1501 ggcattgccc ccaccaaggc caagcgccgc gtggtgcagc gcgagaagcg cgccgtgggc
1561 atcgggcgcc tgttctggg ctctctggg gccgccggca gcacctggg cgccgccagc
1621 atcacctga cgtgcagcg ccgccagctg ctgagcgga tcgtgcagca gcagagcaac
1681 ctgctgaagg ccatcgaggc ccagcagcac atgtgcagc tgaccgtgtg gggcatcaag
1741 cagctgcagg cccgctgct ggccatcgag cgctacctga aggaccagca gctgctgggc
1801 atctggggct gcagcgccg cctgatctgc accaccgccc tgccctggaa cagcagctgg
1861 agcaacaaga gcgagaagga catctgggac aacatgacct ggatgcagtg ggaccgcgag
1921 atcagcaact acaccggcct gatctacaac ctgctggagg acagccagaa ccagcaggag
1981 aagaacgaga aggacctgct ggagctggac aagtgaaca acctgtggaa ctggttcgac
2041 atcagcaact ggccctggtg catctaactc gag

FIGURE 102

NefD125G_TV2_C_ZAopt (SEQ ID NO:134)

ATGGGCGGCAAGTGGAGCAAGAGCAGCATCATCGGCTGGCCCGAGGTGCGC
GAGCGCATCCGCCGCACCCGCAGCGCCGCCGAGGGCGTGGGCAGCGCCAGC
CAGGACCTGGAGAAGCACGGCGCCCTGACCACCAGCAACACCGCCCACAAC
AACGCCGCCTGCGCCTGGCTGGAGGCCCAGGAGGAGGAGGGCGAGGTGGGC
TTCCCCGTGCGCCCCCAGGTGCCCCTGCGCCCCATGACCTACAAGGCCGCCAT
CGACCTGAGCTTCTTCCTGAAGGAGAAGGGCGGCCTGGAGGGCCTGATCTAC
AGCAAGAAGCGCCAGGAGATCCTGGACCTGTGGGTGTACAACACCCAGGGC
TTCTTCCCCGGCTGGCAGAACTACACCCCCGGCCCCGGCGTGCGCTTCCCCCT
GACCTTCGGCTGGTACTTCAAGCTGGAGCCCGTGGACCCCCGCGAGGTGGAG
GAGGCCAACGAGGGCGAGAACAACCTGCCTGCTGCACCCCATGAGCCAGCAC
GGCATGGAGGACGAGGACCGCGAGGTGCTGCGCTGGAAGTTCGACAGCACC
CTGGCCCGCCGCCACATGGCCCGCGAGCTGCACCCCGAGTACTACAAGGACT
GCTGA

FIGURE 103

105040-52566860

NefD125G-Myr_TV2_C_ZAopt (SEQ ID NO:135)

ATGGCCGGCAAGTGGAGCAAGAGCAGCATCATCGGCTGGCCCGAGGTGCGC
GAGCGCATCCGCCGCACCCGCAGCGCCGCCGAGGGCGTGGGCAGCGCCAGC
CAGGACCTGGAGAAGCACGGCGCCCTGACCACCAGCAACACCGCCCCACAAC
AACGCCGCCTGCGCCTGGCTGGAGGCCCAGGAGGAGGAGGGCGAGGTGGGC
TTCCCCGTGCGCCCCCAGGTGCCCTGCGCCCCATGACCTACAAGGCCGCCAT
CGACCTGAGCTTCTTCCTGAAGGAGAAGGGCGGCCTGGAGGGCCTGATCTAC
AGCAAGAAGCGCCAGGAGATCCTGGACCTGTGGGTGTACAACACCCAGGGC
TTCTTCCCCGGCTGGCAGAACTACACCCCGGCCCGGCGTGCGCTTCCCCCT
GACCTTCGGCTGGTACTTCAAGCTGGAGCCCGTGGACCCCGCGAGGTGGAG
GAGGCCAACGAGGGCGGAGAACAACCTGCCTGCTGCACCCCATGAGCCAGCAC
GGCATGGAGGACGAGGACCGCGAGGTGCTGCGCTGGAAGTTCGACAGCACC
CTGGCCCGCCGCCACATGGCCCGCGAGCTGCACCCCGAGTACTACAAGGACT
GCTGA

FIGURE 104

105040" 52565550

↓: is the regions for β -sheet deletions

*: is the N-linked glycosylation sites for subtype C TV1 and TV2. Possible mutation (N \rightarrow Q) or deletions can be performed.

		1		50
SF162	(1)	----MDAMKRGLCCVLLCGAVFVSPSAVEKLVVTVYYGVPVWKEATTTTL		
TV1.8_2	(1)	MRVMGTQKNCQQWWIWGILGFWMLMICNTEDLVVTVYYGVPVWRDAKTTTL		
TV1.8_5	(1)	MRVMGTQKNCQQWWIWGILGFWMLMICNTEDLVVTVYYGVPVWREAKTTTL		
TV2.12-5/1	(1)	MRARGILKNYRHHWWIWGILGFWMLMNCNVKGLVTVYYGVPVVGREAKTTTL		
Consensus	(1)	MRVMGTQKNCQQWWIWGILGFWMLMICNVEDLVVTVYYGVPVWREAKTTTL		
		51	*	100
SF162	(47)	FCASDAKAYDTEVHNWATHACVPTDPNPQEI VLE NV TEN FNMWKNNMVE		
TV1.8_2	(51)	FCASDAKAYETE VHNWATHACVPTDPNPQEI VLG NV TEN FNMWKNDMAD		
TV1.8_5	(51)	FCASDAKAYETE VHNWATHACVPTDPNPQEI VLG NV TEN FNMWKNNMAD		
TV2.12-5/1	(51)	FCASDAKAYEKE VHNWATHACVPTDPNPQEI VLG NV TEN FNMWKNDMVD		
Consensus	(51)	FCASDAKAYETE VHNWATHACVPTDPNPQEI VLG NV TEN FNMWKNNMVD		
		101	$\beta 2 / V 1 V 2 / \beta 3$	*
			↓	
SF162	(97)	QM HEDIISLWDQSLKPCVKLTPLCVTLHCTNLK NATNTK-----SSN---		
TV1.8_2	(101)	QM HEDVISLWDQSLKPCVKLTPLCVTLNCTDNTVTGNRTVTGNSTNTNNG		
TV1.8_5	(101)	QM HEDIISLWDQSLKPCVKLTPLCVTLNCTDNTVTGNRTVTGNNDTNIA		
TV2.12-5/1	(101)	QM QEDIISLWDQSLKPCVKLTPLCVTLNCTNATVNYN-----NTS---		
Consensus	(101)	QM HEDIISLWDQSLKPCVKLTPLCVTLNCTNTNTVTGNRTVTGNSNSN A		
		151	*	*200
SF162	(139)	WKEMDRGEIKNCSEKVTTSIRNKMQKEYALFYKLDVVPIDN----DNTSY		
TV1.8_2	(151)	TGIYNIEMKNCSEFNATTEL RDKKHKEYALFYRLDIVPLN--ENS DNFTY		
TV1.8_5	(151)	NATYKYEMKNCSEFNATTEL RDKKHKEYALFYKLDIVPLN--ENS NNFTY		
TV2.12-5/1	(141)	-----KDMKNCSEFYVTTEL RDKKKKENALFYRLDIVPLNNRKNGNINNY		
Consensus	(151)	A Y EEMKNCSEFNVTTEL RDKKHKEYALFYKLDIVPLNN ENS NNFTY		
		201	*	*
			↓	
SF162	(185)	KLINCNTSVITOACPKVSFEPIPIHYCAPAGFAILKCNDKKFNGSGPCTN		
TV1.8_2	(199)	RLINCNTSTITOACPKVSFDPIPIHYCAPAGYAILKCNNKTFNGTGPCYN		
TV1.8_5	(199)	RLINCNTSTITOACPKVSHDPIPIHYCAPADYAILKCNNKTFNGTGPCYN		
TV2.12-5/1	(185)	RLINCNTSALTTOACPKVSFDPIPIHYCAPAGYAPLKCNNKKFNGIGPCDN		
Consensus	(201)	RLINCNTSTITOACPKVSFDPIPIHYCAPAGYAILKCNNKTFNGTGPCYN		
		251	*	*
			↓	
SF162	(235)	VSTVQCTHGIRPVVSTQLLNGSLAEEGVVIRSENFTDNAKTIIVQLKES		
TV1.8_2	(249)	VSTVQCTHGIRPVVSTQLLNGSLAEEGIIIRSENLTENTKTIIVHLNES		
TV1.8_5	(249)	VSTVQCTHGIRPVVSTQLLNGSLAEEGIIIRSENLTENTKTIIVHLNES		
TV2.12-5/1	(235)	VSTVQCTHGIRPVVSTQLLNGSLAEEIIIRSENLTNNVKTIIIVHLNES		
Consensus	(251)	VSTVQCTHGIRPVVSTQLLNGSLAEEGIIIRSENLTENTKTIIVHLNES		
		301*	*	*350
SF162	(285)	VEINCTRPNNNTRKSIITIGPGRAFATGDIIGDITROAHCNISGEKWNTL		
TV1.8_2	(299)	VEINCTRPNNNTRKSVRIGPGQAFYATNDVIGNTROAHCNISTDRWNKTL		
TV1.8_5	(299)	VEINCTRPNNNTRKSVRIGPGQAFYATNDVIGNTROAHCNISTDRWNKTL		
TV2.12-5/1	(285)	IEIKCTRPNNNTRKSVRIGPGQAFYATGDIIGDITROAHCNISKNEWNTL		
Consensus	(301)	VEINCTRPNNNTRKSVRIGPGQAFYATNDIIGNITROAHCNISTDRWNKTL		

FIGURE 105A

		351	*		*	400	*
SF162	(335)	KQIVTKLQAQFGNKT-	IVFKQSSGGDPEI	VMHSFNCGGEFFYC	NSTQLFN		
TV1.8_2	(349)	QQVMKKLGEHFPNKT-	IQFKPHAGGDLEIT	MHSFNCRGEEFYCN	TSNLFN		
TV1.8_5	(349)	QQVMKKLGEHFPNKT-	IKFEPHAGGDLEIT	MHSFNCRGEEFYCN	TSNLFN		
TV2.12-5/1	(335)	QRVSQKLQELEFPNST	GIKFAPHSGGDLEI	TTHSFNCGGEEFYCN	TTDLFN		
Consensus	(351)	QQVMKKLQEHFPNKT	IKFKPHAGGDLEIT	MHSFNCRGEEFYCN	TSNLFN		
		401	*	*		450	
SF162	(384)	STWNN-----	TIGPN-NTNGTITL	PCRIKQIINRWQEV	GKAMYAPPIRG		
TV1.8_2	(398)	STYHS---	NNQTYKNGNSSSPIT	LQCKIKQIVRMWQV	GQATYAPPIAG		
TV1.8_5	(398)	STYYP---	KNGTYKNGNSSLPIT	LQCKIKQIVRMWQV	GQAMYAPPIAG		
TV2.12-5/1	(385)	STYSNGTCTNCT	CMSEN--NTERITLQ	CRKQIINRWQEV	GRAMYAPPIAG		
Consensus	(401)	STYHN	NGTYKNGNSS	PITLQCKIKQIIR	MWQVGQAMYAPPIAG		
		451	*	*	*	500	
SF162	(427)	QIRCSSNITGLLL	TRDGGKEISNT--	TEIFRPGGGDMRD	NWRSELYKYKV		
TV1.8_2	(445)	NITCRSNITGILL	TRDGGFNNTNN--	TETFRPGGGDMRD	NWRSELYKYKV		
TV1.8_5	(445)	NITCRSNITGILL	TRDGGFNNTNND	TEETFRPGGGDMRD	NWRSELYKYKV		
TV2.12-5/1	(433)	NITCRSNITGILL	TRDGGDNNTET--	ETFRPGGGDMRD	NWRSELYKYKV		
Consensus	(451)	NITCRSNITGILL	TRDGGFNNTNT	TETFRPGGGDMRD	NWRSELYKYKV		
		501				550	
SF162	(475)	VKIEPLGVAPT	KAKRRVVQREKRA	VTLGAMFLGFLGA	AGSTMGARSLT	LT	
TV1.8_2	(493)	VEIKPLGIAPT	KAKRRVVQREKRA	VGIGAVFLGFLGA	AGSTMGAASIT	LT	
TV1.8_5	(495)	VEIKPLGIAPT	KAKRRVVQREKRA	VGIGAVFLGFLGA	AGSTMGAASIT	LT	
TV2.12-5/1	(480)	VEIKPLGVAPT	AAKRRVVEREKRA	VGIGAVFLGFLGA	AGSTMGAASIT	LT	
Consensus	(501)	VEIKPLGIAPT	KAKRRVVQREKRA	VGIGAVFLGFLGA	AGSTMGAASIT	LT	
		551				600	
SF162	(525)	VQARQLLSGIV	QQQNNLLRAIEA	QOHLLOLTVWGI	KQLOARVLAVER	YK	
TV1.8_2	(543)	VQARQLLSGIV	QQQSNLLKATEA	QOHLLOLTVWGI	KQLOARVLAIER	YK	
TV1.8_5	(545)	VQARQLLSGIV	QQQSNLLKATEA	QOHLLOLTVWGI	KQLOARVLAIER	YK	
TV2.12-5/1	(530)	VQARQLLSGIV	QQQSNLLRAIEA	QOHLLOLTVWGI	KQLOARVLAIER	YK	
Consensus	(551)	VQARQLLSGIV	QQQSNLLKATEA	QOHLLOLTVWGI	KQLOARVLAIER	YK	
		601		*	*	650	*
SF162	(575)	DQQLLGIWGC	SGKLICTTAVP	WNASWSNKS	LDQIWNMTWM	EWEREIDNY	
TV1.8_2	(593)	DQQLLGIWGC	SGRLICTTAVP	WNSSWSNKSE	KDIWDNMTWM	QWDREISNY	
TV1.8_5	(595)	DQQLLGIWGC	SGRLICTTAVP	WNSSWSNKSE	ADIWDNMTWM	QWDREINNY	
TV2.12-5/1	(580)	DQQLLGIWGC	SGKLICTTNV	LWNSSWSNK	TOSDIWDNMTWM	QWDREISNY	
Consensus	(601)	DQQLLGIWGC	SGKLICTTAVP	WNSSWSNKSE	ADIWDNMTWM	QWDREISNY	
		651				700	
SF162	(625)	TNLIYTLIEES	QNQOEKNEQELLE	LDKWNWFDISK	WLWYIKIFIMI		
TV1.8_2	(643)	TGLIYNLLED	SQNQOEKNEKDLLE	LDKWNWFDISN	WYIKIFIMI		
TV1.8_5	(645)	TETIFRLLED	SQNQOEKNEKDLLE	LDKWNWFDISN	WYIKIFIMI		
TV2.12-5/1	(630)	TNTIYRLLED	SQSQOEKNEKDL	LALDRWNWFSIT	NWYIKIFIMI		
Consensus	(651)	TNTIYRLLED	SQNQOEKNEKDLLE	LDKWNWFDISN	WYIKIFIMI		
		701				750	
SF162	(675)	VGGLVGLRIV	FTVLSIVNRV	QGYSPLSFQTR	FPAPRGPD	RPEGIEEEGG	
TV1.8_2	(693)	VGGLIGLRII	FAVLSIVNRV	QGYSPLSFQTL	TPSPRGD	RDLGGIEEEGG	
TV1.8_5	(695)	VGGLIGLRII	FAVLSIVNRV	QGYSPLSFQTL	TPSPRGD	RDLGGIEEEGG	
TV2.12-5/1	(680)	VGGLIGLRII	FAVLSIVNRV	QGYSPLSQTL	IPNPRGD	RDLGGIEEEGG	
Consensus	(701)	VGGLIGLRII	FAVLSIVNRV	QGYSPLSFQTL	TPSPRGD	RDLGGIEEEGG	

FIGURE 105B

		751		800
SF162	(725)	ERDRDRSSPLVHGLDALIWDDLRSICLFSYHRLRDLILIAARIVELLGR-		
TV1.8_2	(743)	EQDRDRSIRLVSGFLSLAWDDLRLNLCFSYHRLRDFILIAVRAVELLGHS		
TV1.8_5	(745)	EQDRDRSIRIVSGFLSLAWDDLRSICLFSYHRLRDFILIAVRAVELLGHS		
TV2.12-5/1	(730)	EQDSSRSIRLVSGFLTLAWDDLRSICLFCYHRLRDFILIVVRAVELLGHS		
Consensus	(751)	EQDRDRSIRLVSGFLSLAWDDLRSICLFSYHRLRDFILIAVRAVELLGHS		
		801		850
SF162	(774)	-----RGWEALKYWGNELOYWIOELKNSAVSLFDAIAIAVAEGTDRIIE		
TV1.8_2	(793)	SLRGLQRGWEILKYLGLSLVOYWGLELKKSAISLLDTIAITVAEGTDRIIE		
TV1.8_5	(795)	SLRGLQRGWEILKYLGLSLVOYWGLELKKSAISPLDTIAIAVAEGTDRIIE		
TV2.12-5/1	(780)	SLRGLQRGWGTLLKYLGLSLVOYWGLELKKSAINLLDTIAIAVAEGTDRIIE		
Consensus	(801)	SLRGLQRGWEILKYLGLSLVOYWGLELKKSAISLLDTIAIAVAEGTDRIIE		
		851		876
SF162	(818)	VAQRIGRAFLHIPRRIRQGFERALL-		
TV1.8_2	(843)	LVQRICRAILNIPRRIRQGFEEAALL-		
TV1.8_5	(845)	LVQRICRAILNIPRRIRQGFEEAALL-		
TV2.12-5/1	(830)	FIONLCRGIRNVPRRIRQGFEEAALQ-		
Consensus	(851)	LVQRICRAILNIPRRIRQGFEEAALL		

FIGURE 105C